

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 2, 2000, 14:54:45 ; Search time 10764.3 Seconds
(without alignments)
2150.454 Million cell updates/sec

Title: US-09-358-322-1
Perfect score: 5300
Sequence: 1 gatcaataataatgaaccca.....taccatttacttaactgac 5300

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues 2067340
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl.*
- 1: gb_ba1.*
- 2: gb_ba2.*
- 3: gb_om.*
- 4: gb_ov.*
- 5: gb_pat.*
- 6: gb_ph.*
- 7: gb_pl1.*
- 8: gb_pl2.*
- 9: gb_pl3.*
- 10: gb_pr1.*
- 11: gb_pr2.*
- 12: gb_pr3.*
- 13: gb_ro.*
- 14: gb_sy.*
- 15: gb_un.*
- 16: em_fun.*
- 17: em_hum1.*
- 18: em_hum2.*
- 19: em_in.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sy.*
- 28: em_un.*
- 29: em_v1.*
- 30: gb_ba3.*
- 31: gb_in1.*
- 32: gb_in2.*
- 33: gb_in3.*
- 34: gb_pl3.*
- 35: gb_pr4.*
- 36: em_ba1.*
- 37: em_ba2.*
- 38: em_bt1.*
- 39: em_bt2.*
- 40: em_bt3.*
- 41: em_bt4.*
- 42: em_bt5.*
- 43: em_bt6.*

- 44: em_bt7.*
- 45: em_bt8.*
- 46: em_bt9.*
- 47: em_bt10.*
- 48: em_bt11.*
- 49: em_bt12.*
- 50: em_bt13.*
- 51: em_bt14.*
- 52: em_bt15.*
- 53: em_bt16.*
- 54: em_bt17.*
- 55: em_bt18.*
- 56: em_bt19.*
- 57: em_bt20.*
- 58: em_bt21.*
- 59: em_bt22.*
- 60: em_bt23.*
- 61: em_hum3.*
- 62: em_hum4.*
- 63: em_hum5.*
- 64: em_hum6.*
- 65: gb_pr5.*
- 66: gb_pr6.*
- 67: gb_pr7.*
- 68: gb_bt1.*
- 69: gb_bt2.*
- 70: gb_bt3.*
- 71: gb_bt4.*
- 72: gb_bt5.*
- 73: gb_bt6.*
- 74: gb_bt7.*
- 75: gb_bt8.*
- 76: gb_bt9.*
- 77: gb_bt10.*
- 78: gb_bt11.*
- 79: gb_bt12.*
- 80: gb_bt13.*
- 81: gb_bt14.*
- 82: gb_bt15.*
- 83: gb_bt16.*
- 84: gb_bt17.*
- 85: gb_bt18.*
- 86: gb_bt19.*
- 87: gb_bt20.*
- 88: gb_bt21.*
- 89: gb_bt22.*
- 90: gb_bt23.*
- 91: gb_sts1.*
- 92: gb_sts2.*
- 93: gb_vil.*
- 94: gb_vil2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	314.6	5.9	1306	2	CRPCS20
2	155.2	2.9	312430	2	RPIX02
3	149.2	2.8	14001	33	PFCOMP1RB
4	144.8	2.7	69034	31	AF007261
5	140.6	2.7	317511	2	CJ11168X3
6	138.2	2.6	19517	33	DMU37541
7	137.6	2.6	4601	33	DMU11584
8	136.2	2.6	104992	68	AC005504
9	136.2	2.6	163226	68	AC004157
10	133.2	2.5	14867	31	AE001398
11	128.4	2.4	86827	33	PFMAL3P5
12	124.2	2.3	86827	33	PFMAL3P5

```
13 123.8 2.3 67970 33 PFMAL1P3
C 14 123.6 2.3 4601 33 DMU11584
C 15 123.6 2.3 19517 33 DMU37541
C 16 120 2.3 161891 68 AC008206
C 17 119.4 2.3 104992 68 AC005504
C 18 119.4 2.3 163226 68 AC004157
C 19 117.6 2.2 161891 68 AC008206
C 20 110.8 2.1 15421 33 PFCEMP1RA
C 21 110 2.1 75076 9 AC004948
C 22 108 2.0 106650 10 AC007708
C 23 107.8 2.0 67970 33 PFMAL1P3
C 24 107.6 2.0 1275 66 HSU79270
C 25 107.6 2.0 2676 11 AF044321
C 26 106 2.0 2426 34 SDU49822
C 27 105.8 2.0 234112 33 PFMAL1P2
C 28 104.4 2.0 128779 65 HS29K1
C 29 104.4 2.0 145670 10 AC008132
C 30 104.4 2.0 187543 10 AC005678
C 31 100.6 1.9 1496 32 CEY53C12D
C 32 100.6 1.9 242893 90 CEY53C12
C 33 99.8 1.9 298987 31 AE003846
C 34 99.4 1.9 17443 32 CEY52E8A
C 35 99.2 1.9 12900 31 AE001429
C 36 99.2 1.9 122364 10 AC007324
C 37 99.2 1.9 159550 71 AC013360
C 38 99.2 1.9 170102 10 AC008079
C 39 98.8 1.9 321003 90 PFMAL1P3
C 40 98.4 1.9 8514 34 SPAC1420
C 41 98.4 1.9 94384 11 AC011718
C 42 98.4 1.9 208684 83 AC027048
C 43 96.8 1.8 124760 35 AC011355
C 44 96.8 1.8 173915 35 AP001254
C 45 96.8 1.8 340000 35 AP001678
```

```
/transl_table=11
/protein_id="CAA41197.1"
/db_xref="GI:40640"
/db_xref="SPTREMBL:Q04302"
/translation="MTOKAKNTIYLLILILMLCLVYASVPLYSFCKVTGVTGVTNR
TTIVTQSKGKTIKIRFNADINKELPWKFYEIPYTTVKPGEQKLIYFRAENLNEY
VSGMAVYNTPYKGYFNKVFACFCFTKOTLSPYOKTIMPVFFIDQVIIN"
BASE COUNT 533 a 204 c 183 g 386 t
ORIGIN
```

Query Match 5.9%; Score 314.6; DB 2; Length 1306;
Best Local Similarity 80.5%; Pred. No. 2.4e-28;
Matches 368; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

```
QY 5 aaataaaataaaccagaataaagaacactattttaggttaataagcaataatactatc 64
DB 710 AATAAATAACACAAAACCAAAATACTATCTATTATTATTAATATCATCTACTATC 769
QY 65 tatgatattgttagtgaacgactctctgtaccactatatagtatttttgtaaaagtaacagg 124
DB 770 TATGTTATGTTTAGTATATGCTTCAGTACCATTATACAGCATATTCCTGTAAGTTACAGG 829
QY 125 ttatgaggtacagtaagaacaagtaataataataataataataataataataataataata 184
DB 830 ATACGGAGGAACCTGTCAGAACAACTACAGTAACACAACTCTAACTCGGTAAAGTACTACCAT 889
QY 185 taaagtcagatttaagtcagatatatacaacaacacgcatgcaaaattctctccagaagt 244
DB 890 TAAATAAAGATTAAATGACACATAAATAAAGAACTCCATGGAATAATTTATCTGGAAT 949
QY 245 atctcatgtatttgaacacccagagagaacaaaattgattttaccgcgcagaaaaatct 304
DB 950 ACCTTATACAACTGTCAACACGAGGAGAACAAAATAATTAATTTTATAGACAGAAAAATTT 1009
QY 305 actgtatgaggacacttcaggaaatgctgtatataatgtttacacacacataaagtaggaaa 364
DB 1010 AACTAATGAATACGCTGTACAGGTATGGCTGTATATAATATTGTTACCCCTTACAAAGTAGTAA 1069
QY 365 atatttaataaggtagctgtttttgtttccaccaacaacacataacccctcatcaaaa 424
DB 1070 ATATTTCAATAAGTAGCTGCTGCTGCTTTTACCAACAACAGCTTATCTCTTATCAAAA 1129
QY 425 aactataatgccagatcatcttttttatagatccagcc 461
DB 1130 AACTATTATGCCGTATCATTTTTTTTATAGATCAAGTC 1166
```

RESULT 2

```
RPXX02 312430 bp DNA BCT 12-NOV-1998
LOCUS Rickettsia prowazekii strain Madrid E, complete genome; segment 2/4
DEFINITION AJ235271 AJ235269
VERSION AJ235271.1 GI:3868717
KEYWORDS complete genome.
SOURCE Rickettsia prowazekii.
ORGANISM Rickettsia prowazekii.
Bacteria: Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsiinae; Rickettsia; typhus group.
1 (bases 1 to 312430)
Andersson, S.G., Zomorodipour, A., Andersson, J.O.,
Sicheritz-Ponten, T., Alsmark, U.C., Podowski, R.M., Naslund, A.K.,
Eriksson, A.S., Winkler, H.H. and Kurland, C.G.
The genome sequence of Rickettsia prowazekii and the origin of
mitochondria
Nature 396 (6707), 133-140 (1998)
99039499
REFERENCE 2 (bases 1 to 312430)
AUTHORS Andersson, S.G.E.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1998) S.G.E. Andersson,
Siv.Andersson@molbio.uu.se, Dept. of Molecular Biology, University
```

ALIGNMENTS

```
RESULT 1
CRPCS20 1306 bp DNA BCT 30-JUN-1993
LOCUS C.ruminantium (clone pCS20) DNA for unknown ORF.
DEFINITION X58242.1 GI:40639
ACCESSION X58242.1 GI:40639
VERSION X58242.1 GI:40639
KEYWORDS unidentified open reading frame.
SOURCE heartwater rickettsia.
ORGANISM Cowdria ruminantium
Bacteria: Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Cowdria.
1 (bases 1 to 1306)
McGuire, T.C.
Direct Submission
Submitted (08-MAR-1991) T.C. McGuire, Washington State University,
Dept. of Vet-Micro/Pathology, Bustad Hall, Pullman WA 99164-7040,
USA
2 (bases 1 to 1306)
Waghela, S.D., Rurangirwa, F.R., Mahan, S.M., Yunker, C.E.,
Crawford, T.B., Barbet, A.F., Burridge, M.J. and McGuire, T.C.
A cloned DNA probe identifies Cowdria ruminantium in Amblyomma
variegatum ticks
J. Clin. Microbiol. 29 (11), 2571-2577 (1991)
92129532
COMMENT See also X58243.
FEATURES Location/Qualifiers
source 1..1306
/organism="Cowdria ruminantium"
/strain="Crystal Springs (zimbabwe)"
/db_xref="taxon:779"
/clone.lib="genomic: E.coli pUC 19"
/clone="PCS20"
717..1178
/note="unknown ORF"
/codon_start=1
CDS
```

COMMENT FEATURES source	of Uppsala, Husargatan 3, Uppsala, S-751 24, SWEDEN On Nov 13, 1998 this sequence version replaced gi:3860789.	
	Location/Qualifiers	
	1. .312430	
	/organism="Rickettsia prowazekii" /strain="Madrid E" /db_xref="taxon:782" 76. .1830 /gene="RP226" 76. .1830 /gene="RP226" /codon_start=1 /transl_table=11 /product="unknown" /protein_id="CAAL4691.1" /db_xref="GI:3860789"	
gene	/translation="MLNKLCDILFLINLLTVQYASPPPLPSPSLPIIAYDVTDKNI STNSIEFEKFEKQKKNISSEHOEQTKAIHOESQIDISRELNENEQSEPEFI DFGSTITLSVASNIDSKAEYENSTNLAASNTQIQVQKEFPSEASEPIDGNTK FTSATNHEMYKEAVSSNDKETNLSTNIITPNVPVISIPTAQDNYVYVPSQSVQIY KPTNLTSIRNPILNHLNDEKNEKNLESTISNTTPTTNMVSVPISQDTIOTTLNIT VPTAEHTVSQVTSVTHMSNOHSAQPIPTISINTPVTSTVLRSATESSVPINNQEIF VSESETKQDQWYTPIMPLVVDPNKQSKPLALEQKNNDQIINNOAESHSVSSNV TIOKQDNVNAATSESTKEFKVNETQMLFLPDDDIVLGKLTEDATLEQMDMHGKILP OKKEWIANAKRKLVSFIKYYDDINKKDIYANLSYSAVDNAFRAVENNNLFELR ALLDVPILQAKNSTGETLLTSSYNGNYILAKFLVIRGITSVLKNDCKEYPLDIAL AKGNTNIVCMMLKAKGN"	
gene	2025. .4013 /gene="RP227" 2025. .4013 /gene="RP227" /codon_start=1 /transl_table=11 /product="DNA GYRASE SUBUNIT B (gyrB)" /protein_id="CAAL4690.1" /db_xref="GI:3860790"	
CDS	/translation="MSDLFSLNKEKKKIVITNYSAKDIEVLGDELPVVRKPGWYIG TDSNAMHLVSELDNDMEAVAGFASIIIMKHODHSITIFDNGRGIPIDNHKFPD KSALEVITLTTHSGSKSNVYHTSGGLHGVGISVYNALSKHFKIKVYKQGLKYSQY SKGAKVTLDSAEASKRGRGTSINFTPDPEIFSEKLNHPKKIYEIARSKAYLRGVG IEWECEVLPDIPKALINPGLKDYLSKKISLDNLVPIEISGNIESTVDDIKLE WAICWQNDTSAPQSCVNTVPTFGGTHEOGLKSAILRGLKAYSEMIGNKKAANLTI EDILETASIVLSIFIVEFSGQTKERKLVSGVSKLVENIIRKDFHFLSDSKVLATH LLEHVIAIEFRNNKKNERNISRSVTKRLPGKLADCTRSAGTELFIVEGDSAG GSAQKARNRETQAVLPWGLVNLVSTLEKIIINNOAQIDLEIALACGSLKNYKKNEL RYEKIITMDADVDGAHTASLNTFFFLRMPKLVEEGHLYLAKPLVRLTOSNKIYVA CDEEKIKLYTKLSKAKAKTEVGRFGKLGEMPAQLKETTMMHPEKRSLLKVTLEDVQ NVDKIVDLMSKKPEKRFQFIYEQALVKMDQIINKLDI" 4122. .5447 /gene="RP228" 4122. .5447 /gene="RP228" /codon_start=1 /transl_table=11 /product="TAIL-SPECIFIC PROTEASE PRECURSOR (ctp)" /protein_id="CAAL4691.1" /db_xref="GI:3860791"	
gene	/translation="MLLRFIITLFLSINCATGKETENKISNOEAYKQFQDVEERIEK DYQVPPROKMDIANGMLSLDPSHNYTDELEDIFTTKGEFGGIGVEIWDSC AKIISIDDDLPARAGLGGDIYGVNDELSTLPGPKAKEMRGPVTKVRLIIR EEEAQPOLETRIEIKPIKAHLEKNNIAYIRITTFNESTISLKAARVKKLTKES DNLRGIILDLNAGGILDQAIYSDYFIDSGVITVTKGRTTSNSETKANEFSLKAP KVMPLVINGSASSETVAGALQDHKRAIILGTSGFGKGSVQALTOINSRAAVKLTI SKYVTPSGRSIQAEIGEPDILIEPAKVEYPEVKIDKREFSESSLKYLKNDNAKNKDS NKEKTKNNKKESESELSLYKKDQPARAYDVIIGLIINTNLETQGRAK" 5653. .7146 /gene="RP229" 5653. .7146 /gene="RP229" /codon_start=1 /transl_table=11 /product="HISTIDINE KINASE SENSOR PROTEIN (barA)" /protein_id="CAAL4692.1"	
gene	/translation="MNNKVIIVRLSFIILFINIVINMLFYRYFMIKEMIKIQAVALHT KIVELYTDNIWNHKNISKYKHKFDYKLQDQDFINFKITAOFTNLNINISYDL LGNKFIITSMMLHSDVNYKDSLEIETVITKIDFLKFTSAAPLRAFGKITSIL LKPVIENESDLTIEHASFVTSYIPVIDHNLDPDVAVEINTNITSOAKNITSLEOK VFYFIIFIIFCIITISNTNAYARQIIEEQLETHRNLAQIEKVEKTSSTNTKFPANI SHEURTPNALIGFSEILMSRDEKSNKIINDHAGKHLSSINDLRLKASADK LKVDNIDDLNKLSSILIKPRAYQAEVLIIRLPRKHVVIINADPRKLKQVNLNL SNAYFTNSGGSVTSILEKDELAKLVYKIDGTIGIGIEKDIPTLSAFQTDSLSLR KYEGTGLGLPLTKKLVELMNGKFDLQSKINKKGTVTITFKYDGSIEI" 7374. .8126 /gene="RP230" 7374. .8126 /gene="RP230" /codon_start=1 /transl_table=11 /product="unknown" /protein_id="CAAL4693.1" /db_xref="GI:3860793"	
CDS	/translation="MKLIILLITFLSFLSGKSEMPQGLKAYVNNDFENRLDEQE QEIRKLKGVILQHKIDKLLQKNLMLNQEENIEVLEDFKQDIFDALLLEGHND VSKRTFEVNDIAPYQAYDLAAYKDNKLEAKDFKFNFIQKYPNNSLSNAYFWY ACECFKQDYNGAAINVLYCKYKESPKGAKSSDGLLKLALSIGELKKMQEACNILAKLD KEFPINTSVSKKMTEDAKIKFGCKINKNNKI" 8123. .8785 /gene="RP231" 8123. .8785 /gene="RP231" /codon_start=1 /transl_table=11 /product="unknown" /protein_id="CAAL4694.1" /db_xref="GI:3860794"	
gene	/translation="MTDILDEVSDQNEKRLIFFKLVPIIIISIVITIMVIRK NKDNRIKNNQKNGDILVKTIGLDTKONKALAFNTLENLITSSNTKIKEIAALEQVAI RMSKKYLGAKNLLNKIIDNEKYEISITAYARIAWCCIVLDDQSLNIDQDKLQKLYLN YFDDEKPPWATATIIIRAILDKHNMKTQAEKNLKNLASNSDLEKQAKALLVSL SK" 8812. .10059 /gene="RP232" 8812. .10059 /gene="RP232" /codon_start=1 /transl_table=11 /product="unknown" /protein_id="CAAL4695.1" /db_xref="GI:3860795"	
CDS	/translation="MKKKALLLIPFLISCNGLSGSKVKNIVDLTPKLVITQNEPIY LDSNTKIYPFNVNMLKNQYSPAKSMIAEPVFGDMYITLDIRANISAFSEIKNKII WSYNSLKHKKDNYIGGGILHNGKLYITYGARLLIVLDAKSGYIEIRKELPDIIIRKP IALNDHTILVQTIISNOTIALDSETKTLMDHESIAELTSTYSMPIVQHDNVIVYTN TGQVLLNKNKEGVKNFETNLNDHTAIPNFDTSILCTPVDHSMNLYIATGLKLI KLLNLTGSLVQINADDIOSMLIGNSLFIINNARQIAALNPETGKVKFVADLVNRY DKRLKSTFLVPFVGVNDNNQORSNLVISVQDILYNFNIDNSNGLKMNPHIILKINRY YGLRSNNTLYFSTDRQVIFGSI" 10279. .10746 /gene="RP233" 10279. .10746 /gene="RP233" /codon_start=1 /transl_table=11 /product="50S RIBOSOMAL PROTEIN L13 (rplM)" /protein_id="CAAL4696.1" /db_xref="GI:3860796"	
gene	/translation="MKYISAKPSEIEKKWVIDAKNVVLGRLASRVATMLRKKPSP TPHLDCCGNIITINAEHIKLTGKLNLPDGVYIRHFGPGGIDKDTTACKGLSKGYE RVIKMAYKRMITRNVLGAKQNSNLVYVANCEPHMAOQPTIYDFASENPKNKK" 10753. .11238 /gene="RP234" 10753. .11238 /gene="RP234" /codon_start=1 /transl_table=11	

Db	91844	GGTAAGATTGAACATGTTATGAGTAAGATGAGTGT 91877
RESULT	3	
LOCUS	PFCOMP1RB	14001 bp DNA INV 14-FEB-1997
DEFINITION	P.falciparum complete gene map of plastid-like DNA (IR-B).	
ACCESSION	X95276	
VERSION	X95276.1	GI:1171591
KEYWORDS	Clp gene; LSU rRNA gene; ORF105; ORF129; ORF78; ORF91; rpl14 gene; rpl16 gene; rps11 gene; rps12 gene; rps13 gene; rps17 gene; rps19 gene; rps3 gene; rps4 gene; RPS5 gene; rps7 gene; rps8 gene; trna-Asp; trna-Cys; trna-Gln; trna-Glu; trna-Gly; trna-His; trna-Leu; trna-Lys; trna-Met; trna-Phe; trna-Pro; trna-Ser; trna-Thr; trna-Tip; trna-Tyr; tufa gene.	
SOURCE	malaria parasite P. falciparum.	
ORGANISM	Plasmodium falciparum	
REFERENCE	1 (bases 1 to 14001)	
AUTHORS	Wilson,R.J.M., Denny,P.W., Preiser,P.R., Rangachari,K., Roberts,K., Roy,A., Whyte,A., Strath,M., Moore,D.J., Moore,P.W. and Williamson,D.H.	
TITLE	Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium falciparum	
JOURNAL	J. Mol. Biol. 261 (2), 155-172 (1996)	
MEDLINE	96346169	
REFERENCE	2 (bases 1 to 14001)	
AUTHORS	Wilson,R.J.M.	
TITLE	Direct Submission	
JOURNAL	Submitted (23-JAN-1996) R.J.M. Wilson, National Institute for Medical Research, Mill Hill, London NW7 1AA, UK	
COMMENT	Related sequences X90351-X90354 (incl.), and X87630-X87631 (incl.).	
FEATURES	Location/Qualifiers	
Source	1..14001	
	/organism="Plasmodium falciparum"	
	/strain="C10"	
	/db_xref="taxon:5833"	
	/dev_stage="erythrocytic"	
	/note="IR-B half of 35kb circle, putative Plastid DNA"	
rRNA	1..227	
	/gene="LSU rRNA"	
	/product="large subunit ribosomal RNA"	
gene	1..227	
	/gene="LSU rRNA"	
tRNA	242..314	
	/gene="tRNA-Thr"	
	/product="transfer RNA-Thr"	
gene	242..314	
	/gene="tRNA-Thr"	
gene	340..966	
	/gene="rps4"	
CDS	340..966	
	/gene="rps4"	
	/codon_start=1	
	/protein_id="CAA64576.1"	
	/db_xref="GI:1171592"	
	/db_xref="SPTREMBL:Q25804"	
	/translation="MIRFLPKRIKLKLNPFLYLSGKYNKCLNYKYSYEDLKLKFRICYNYCYKYLYLNKIDKNINILYFKLLKLELDLFDLVNIGFRTILQSYRYIKYKNYIVNNINKYNNKNDILFFNNKIKYIILKNLYKYNIIYISNLYKYNFKIYSYNKYFICIFYNEFKIKILNINILNLYIYNDIYI"	
tRNA	981..1053	
	/gene="tRNA-His"	
	/product="transfer RNA-His"	
gene	981..1053	
	/gene="tRNA-His"	
tRNA	1072..1142	
	/gene="tRNA-Cys"	
	/product="transfer RNA-Cys"	
gene	1072..1142	
	/gene="tRNA-Cys"	

/product="30S RIBOSOMAL PROTEIN S9 (rps1)"		
/protein_id="CAA14697.1"		
/db_xref="GI:3860797"		
/translation="MTELKIKTEKVKVLTQKESLKVLPKPKIDSVSKFYATGRRKNAIARVLKVGKIVVNNKILNOYFSETVKTILOPILTKITDIDYDVICVKGGGISQKGAILHGISKALDSACFHAHLKGGLLTRDSRVVERKKYGGKARKKTQPSK R"		
tRNA	11279..11352	
	/gene="tRNA Met (CAT)"	
gene	11279..11352	
	/gene="tRNA Met (CAT)"	
gene	complement(112284..112769)	
	/gene="RP236"	
CDS	complement(112284..112769)	
	/gene="RP236"	
	/codon_start=1	
	/transl_table=11	
	/product="INVASION PROTEIN A (invA)"	
	/protein_id="CAA14698.1"	
	/db_xref="GI:3860798"	
	/translation="MRNSSNKYLDLPYRPGVGMILNADQIFVGGRIKISQWMPQGGIVGPTSPSTAARMLEIGSNKGYIAESKCWYSYDVPSFLIPKLWNGFRGKQKWLIRGTGNKNDIINHTSPEDORWISLDELLSIIPFRKKLQAVVKEFESLI Q"	
gene	complement(12798..14150)	
	/gene="RP237"	
CDS	complement(12798..14150)	
	/gene="RP237"	
	/codon_start=1	
	/transl_table=11	
	/product="unknown"	
Query Match	2.9%; Score 155.2; DB 2; Length 312430;	
Best Local Similarity	55.7%; Pred No. 2,1e-10;	
Matches	320; Conservative 0; Mismatches 248; Indels 6; Gaps 1;	
Qy	15 aaacaagaataagaacactattatgattagtaataagcaataataactatctatgatattgt 74	
Db	91304 AAAAAATCCAATAAAAAATTTAGCCTTTTCATCTTGGGGTTTAATGATGATGATGTTA 91363	
Qy	75 ttsgtgaagctctgtaccacatatagatatattttgtaaaagtaaacagggttatggaagt 134	
Db	91364 TTGAGTTTTCGTCCTACTATATATACTATTATTGTGAAAAGTTACTGGTTATGGTGTG 91423	
Qy	135 acagtaag-----aacagtaataatacaattctcaaaataggtaacactattataa 188	
Db	91424 ACTACTATTAAAGAACAGTTAGTGTATATTCTAGGTAAAGAGTACTAAAGCTATAATT 91483	
Qy	189 gtcagatttaatgcagatatacacaacaactgccatggaaaattctatccagaagtatct 248	
Db	91484 ATTGAGTTTGATCCTAATGTGTATCCAAATCTACCTTGCGATTTTATCCCAAGGCAGAAA 91543	
Qy	249 catgtattttgaaaccacagaggaacaaaaattgattttctaccgcgcagaaaaatctact 308	
Db	91544 AGAGTTCAAAATTCCCGGACAGAGATACACTAGTGTCTCTATGAAGCAGAAAACTTAAGC 91603	
Qy	309 gatgaggacactcagaaatgctgtatataatgtttacaccacataaagtggaaaaaat 368	
Db	91604 AATAAGGATATAATAGTACATCGATATATAATGTTTCTACCTCAAAATAAGCAGGAAATAT 91663	
Qy	369 tttaataaggtagctgtttttgtttccacaacaacattatcaccccatcaaaaaact 428	
Db	91664 TTGCTAAAAATTCATGTGTTTGTGTTGAAGAACAAATTATTAAAGCTAGGAAAAAGTT 91723	
Qy	429 ataatgcagtatcatatttttatagatccagccatagaaacagatccctgaaactctgac 488	
Db	91724 TTAATGCTGTGTACATTTTATATAGATAATGATTTTGAGCGGTGATCCTGAAATGAAAAAC 91783	
Qy	489 gtaaaactcatcactctttcattatgattcttttaagtaacaagaataaaacttcataacc 548	
Db	91784 ATTAAGATAATTACTTTATCTTATCTTTTAAAAATAAGAAATATTAGCTGGAATAC 91843	
Qy	549 gtacattataactgtatataaaaaataactatt 582	

Db	5807	TATAAATTTATTACACATATATTAGCTTTAAANAATATAAAAATGGTGGTATTTATTATT	5866
Qy	2724	tatactctgctcgaatttagctacaaagagaatgaatcaacgcgtatatctcaaaggcc	2783
Db	5867	TATATTG--TAAATATTATAGTTATTAATTTGTATCATTAATAATAGAAGTCACAT	5923
Qy	2784	accatattctacaagaagtacctggcgacattaaaaacacatacataccaaccaggaag	2843
Db	5924	TTTTAAATAATATATAAAGAAGGTAATATATATTTAAATTTTAGATATAAAATATTGA	5983
Qy	2844	acgtgcattatatataaaaatacttttgacaaggaacaataactgcttcagcgcacag	2903
Db	5984	ATTATATATATATTTAAAAATAATAATAGATATATAATTTAAATTTAAATAATA	6043
Qy	2904	gagatgtagtccaacacagcgtcatcaaatctactagataaatactcttccaaattgc	2963
Db	6044	TATATATATTTTATAAAAATATATTTATTTATTTTAAATGCTATPAAAGTATA	6103
Qy	2964	cactggtaatacaaaaaataccataccagatcagcgttgttaatagagaagacacatta-	3022
Db	6104	TATTTAGTAATATATTTAAATAAACATAATATAAAAGTATCAGTTAATTTTAAATATA	6163
Qy	3023	-ttatctgacagagagatgtaccacaagtgctcaatgcttctcagacacagctacc	3081
Db	6164	TTGGTATAAATTTATAAATTTTATATATAAAAAAGGTAATTTTAAATTTCAATATA	6223
Qy	3082	atatcacgcaagactcatcgctcaaacctgtctcaactactgatcgtagcgagattaag	3141
Db	6224	AATATAGTCATAAATAATTTATAGTTACCTAATATAATATTTTGTCAGTTAGATATA	6283
Qy	3142	tctcaattcceaattaatgatgaataagagacaagttaggattacaatactaccatagtag	3201
Db	6284	ATAAAAATTTTATATTTATATAGTATGGATATATTTATTTAAATTCATTGGGAAT	6343
Qy	3202	cagttcactatcaatacaataatgtagtagatattgttaagcttcaaatattcacgataa	3261
Db	6344	TAAATAATTCATTTCCAATATATAAATAAATAAAGAATTAAGGTATAAAAAATTAAT	6403
Qy	3262	taccacagtaacaaaatgatcatcgctctaacagatattatagacacattaaaaagta	3321
Db	6404	GAT--AATTAATATTATTAATAAANNTAAATATTTTATATATTATATTATGTTATA	6461
Qy	3322	-tggaagtgtgaagaacacttttgcgaattgcgaacttagtatcccaactcttttattt	3380
Db	6462	GTATTTTAAAGTATTTTATTTATTTTAAAGAAAGGTTTAATTAATTTTCTAT	6521
Qy	3381	tactatgttaaatacaataatgtagtgagatatgtttaagcttcaaatattcacgatac	3440
Db	6522	AAAAATTTAATATTTTAAATTTATATTTTAAATTTATTTATATATAAATAAAGAGA	6581
Qy	3441	tagatcgagttatataataacaactctctactacaagcaataacaatagaagaag	3500
Db	6582	GATAAAAATATATTTTAAATAAATAAGTAAATTTTATTTTATTTTATTTATAA	6641
Qy	3501	taataaaattgccagaataattctcaatgaattagttaatatgaagtaggagaaaa	3560
Db	6642	TATAATAATAATTTAAGTTAAATAATAGTATTATAAGTTAAATAATAATTTATTGAA	6701
Qy	3561	acaatacaataaattggcaacaataatagatgctaaaaaacacataccttggttaagatac	3620
Db	6702	AAAAATTTTGAAT--AAAAAAAATCTCTTACAAATAAAAAAGGAAATTAGAAGAT	6759
Qy	3621	aggttattgatttactacaagttcttatagggtgtattaaagtaagataaagtagctt	3680
Db	6760	ATAAATATGTTATTAGTATTAGTATTAACAAGGTGGAT-----AGGATTAGAGTTA	6813
Qy	3681	caatcaataaaaaaacattaaccaagttgttagctctaccggagaagcttattataagc	3740
Db	6814	GTAAAGAAATCAATATTANTAAGCTTATTATATCGCTTAATAATAAAGCTTTAAATA	6873
Qy	3741	ttttaacctgggataatatgaagtttctgaattgaagcaaaaaattagtaatacacaat	3800
Db	6874	TTTATTTTAAATTTCTATTTAAATATATAAATAATAAATAAATAAATAATATAATTTAA	6933

Qy	3801	atcaaatctttcttccacgagattatatgttgacctaccataacaacttatatttagaaaaat	3860
Dβ	6934	ATAGTAAATTTTTTTATTAAATACAAATTTAAAATTTTAATTTATTTAAATATAAAGATTTT	6993
Qy	3861	gacaacgagatcacacacatcaataaattatcactcatcattccaattaatcaaaacaacatggta	3920
Dβ	6994	TATTATTAAAAATTTATTTTGAATGTTTAGCTTATTTTAATTTGTAAAATAATAATTTATT	7053
Qy	3921	ttttttaacttaattttaaattttatttttttaaaaataaaaaatacaaattttact	3972
Dβ	7054	ATAATAAPAAACATAAATAGATATAATTTTATTTAAATAAATTTATTATTAAATATT	7105

4

RESULT
AF007261

LOCUS 69034 bp DNA circular INV 03-JUL-2000
Reclinomonas americana mitochondrial DNA, complete genome.

DEFINITION
AF007261

VERSION
AF007261.1 GI:2258325

KEYWORDS

SOURCE
Reclinomonas americana.

ORGANISM
Mitochondrion Reclinomonas americana
Eukaryota; Reclinomonas.

REFERENCE
1 (bases 52095 to 54121)
Burger,G., Lang,B.F., Reith,M. and Gray,M.W.
Genes encoding the same three subunits of respiratory complex II
are present in the mitochondrial DNA of two phylogenetically
distant eukaryotes
Proc. Natl. Acad. Sci. U.S.A. 93 (6), 2328-2332 (1996)
96197311

MEDLINE
2 (bases 67233 to 67344)
Lang,B.F., Goff,L.J. and Gray,M.W.
A 5' S rRNA gene is present in the mitochondrial genome of the
protist Reclinomonas americana but is absent from red algal
mitochondrial DNA
J. Mol. Biol. 261 (5), 407-413 (1996)
96393422

REFERENCE
3 (bases 1 to 69034)
Lang,B.F., Burger,G., O'Kelly,C.J., Cedergren,R., Golding,G.B.,
Lemieux,C., Sankoff,D., Turmel,M. and Gray,M.W.
An ancestral mitochondrial DNA resembling a eubacterial genome in
miniature
Nature 387 (6632), 493-497 (1997)
97311393

MEDLINE
4 (bases 1 to 69034)
Lang,B.F. and Burger,G.
Direct Submission
Submitted (06-JUN-1997) Departement de Biochimie, Universite de
Montreal, 2900 Edouard-Montpetit, Montreal, Quebec H3T 1J4, Canada

JOURNAL
TITLE
Location/Qualifiers
1. 69034
/organism="Reclinomonas americana"
/organelle="mitochondrion"
/strain="ATCC50394"
/db_xref="taxon:48483"
/db_xref="ATCC:50394"
56. .2806
/gene="rnl"
/product="large ribosomal RNA"
56. .2806
/gene="rnl"
2843. .2872
/note="signal element pail"
complement(2923..3006)
/gene="trnL(gag)"
/note="codon recognized: CUC"
/product="tRNA-Leu"
/anticodon=(pos:2971..2973,aa:Leu)
complement(2923..3006)
/gene="trnL(gag)"
complement(3054..3127)
/gene="trnP(uca)"

FEATURES
source

rrna

gene

stem_loop

trna

gene

trna

Matches 291; Conservative 0; Mismatches 192; Indels 21; Gaps 1;			
Qy	50	agcaataactactatcatgatatttagtgtagcctctctaccactatatagtatatt	109
Db	19625	AGCAGTGTCTATTACTATGAGATTTCTTATGGATCTGCTACTCTATATCGTATATT	19684
Qy	110	ttgtaagaatacaggttatgtaggtacagtaagaacaagtaataatcaaatctta----	165
Db	19685	TTGTCAAGTAACTGTTTGGCGGAACAACAACAAGTTGCTGATTAGAAATCAGATATTTT	19744
Qy	166	-----aaataggtacactattattataaagtcagatttaagtcagatat	208
Db	19745	AACATTAAAGATGAACAACAAGAGATAGGATAATACTGTACGTTTAAATGTGATGT	19804
Qy	209	acaaaacaactgcacatggaattctctccagaagtactctcatgtattgtaaaaccagg	268
Db	19805	TAGTGATACATGCTTGGAAATTTTCATCCATACACAAGAAATTAAGTAATGGTGG	19864
Qy	269	agaacaaaaattgtattctaccgcgcagaaatactactgtatgagacacttcaggaa	328
Db	19865	TGAACAGCATTAGCATTTTATTTCAGCAGAAATCCTACGGATTCCTCGATAATTGGTAT	19924
Qy	329	gctgtataataattcacacacataaagtaggaataatttttaagtagctgtttt	388
Db	19925	AAGTACGTATAATGTAAATCCTCAACAGGCAGGTATTTTATTAAGATACAAATGTT	19984
Qy	389	ttgttcaccaacaacattatccctcatcaaaaactataaagtcagtatatttt	448
Db	19985	TTGTTTGAACAACAAGATTAACACATGAACAATAGATGCTGTATTTT	20044
Qy	449	tatagatccagccataaagacagatcctgaaactgctgaactcaaaactcatctttc	508
Db	20045	TATAGATCCTGCAATTTAGATGATCCTAAATGCTGTATATGATCAATAACTTTATC	20104
Qy	509	atatgtattctttaagtacaaga	532
Db	20105	ATATACATTTTAAATGTGAAGA	20128
RESULT 5			
LOCUS	CJ11168X3	317511 bp	DNA BCT 08-JUL-2000
DEFINITION	Campylobacter jejuni NCTC11168 complete genome; segment 3/6.		
ACCESSION	AL13076 AL11168		
VERSION	AL139076.2 GI:6968128		
KEYWORDS	Campylobacter jejuni.		
SOURCE	Campylobacter jejuni.		
ORGANISM	Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group; Campylobacter.		
REFERENCE	1 (bases 1 to 317511)		
AUTHORS	Parkhill,J., Wren,B.W., Mungall,K., Ketley,J.M., Churcher,C., Besham,D., Chillingworth,T., Davies,R.M., Felwell,T., Holtrold,S., Jagels,K., Karlyshev,A., Moule,S., Pallen,M.J., Penn,C.W., Quail,M., Rajandream,M.A., Rutherford,K.M., VanVleet,A., Whitehead,S. and Barrell,B.G.		
TITLE	The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences		
JOURNAL	Nature 403 (6770), 665-668 (2000)		
MEDLINE	20150912		
REFERENCE	2 (bases 1 to 317511)		
AUTHORS	Parkhill,J.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-FEB-2000) Submitted on behalf of the Campylobacter sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk		
COMMENT	Notes: Details of C. jejuni sequencing at the Sanger Centre are available on the World Wide Web. (URL, http://www.sanger.ac.uk/Projects/C_jejuni/). Location/Qualifiers 1. .317511 /organism="Campylobacter jejuni"		
FEATURES	source		

/strain="NCTC 11168"	
/db_xref="taxon:197"	
119..364	gene
/gene="Cj0667"	
119..364	CDS
/gene="Cj0667"	
/note="Cj0667, unknown, len: 81 aa; similar to many hypothetical proteins e.g. YABO_PACSU (86 aa), fasta scores; opt: 149 z-score: 259.2 E(): 3.8e-07, 35.4% identity in 79 aa overlap. 43.6% identity to HP1423"	
/codon_start=1	
/transl_table=11	
/product="hypothetical protein Cj0667"	
/protein_id="CAB72944.1"	
/db_xref="GI:6968129"	
/translation="MRVDKFLNVNITKRRRAISEDCKSGVGVINGVIVKASKEVKVD	
DIITLHFTVYTKYKVLALPSTKSIPKNAQNEVVKL"	
361..768	gene
/gene="Cj0668"	
361..768	CDS
/gene="Cj0668"	
/note="Cj0668, probable ATP/GTP-binding protein, len: 135 aa; similar to hypothetical proteins e.g. XJEE_ECOLI (153 aa), fasta scores; opt: 184 z-score: 205.3 E(): 0.00039, 33.8% identity in 80 aa overlap. 44.2% identity to HP0716. Contains PS00017 ATP/GTP-binding site motif A (P-loop)"	
/codon_start=1	
/transl_table=11	
/product="putative ATP /GTP-binding protein"	
/protein_id="CAB72945.1"	
/db_xref="GI:6968130"	
/translation="MKFILAINEIKTMQIMPEGVVLQGLDASGKTSLVQAVKVF	
LGDVVDVDSPTFTSMOKYENHDICIVHYDIQEGLEGLLANGLFENFEKGLHVEWG	
GNLTKLMKFGISTIQIKISIKDKRKVEIYE"	
442..465	misc_feature
/gene="Cj0668"	
/note="PS00017 ATP/GTP-binding site motif A (P-loop)"	
761..1489	gene
/gene="Cj0669"	
761..1489	CDS
/gene="Cj0669"	
/note="Cj0669, probable ABC-transporter ATP-binding protein, len: 242 aa; highly similar to many e.g. YHBG_ECOLI probable ABC transporter ATP-binding protein (240 aa), fasta scores; opt: 840 z-score: 1144.2 E(): 0, 54.2% identity in 236 aa overlap. 65.8% identity to HP0715. Contains PS00017 ATP /GTP-binding site motif A (P-loop) and Pfam match to entry PF00005 ABC_tran, ABC transporters"	
/codon_start=1	
/transl_table=11	
/product="ABC-transporter ATP-binding protein"	
/protein_id="CAB72946.1"	
/db_xref="GI:6968131"	
/translation="MSKLEIVNLEKIITKIIHGISLVNSGVVLLGPNAGKTT	
TFYIIGLISPSGSKVLGDVTKDPLNKRARGSIGYLPQESSIFKDLSEVDNLLIA	
AQIFYDKKILHDKVEQMLELIEPIRLKGLSLSGERRRCEIARSLMCEPKFLL	
DEPFACVDPIAVAEIOTLKEKLKRLGIVLITDHNVRETLAICDRAVYVIRSGSLASG	
NADEIATNDKVKYILGAEFKLLD"	
845..1396	misc_feature
/gene="Cj0669"	
/note="Pfam match to entry PF00005 ABC_tran, ABC transporters, score 221.60, E-value 1.1e-62"	
866..889	misc_feature
/gene="Cj0669"	
/note="PS00017 ATP/GTP-binding site motif A (P-loop)"	
1486..2718	misc_feature
/note="Pfam match to entry PF00309 Sigma54_factors, Sigma-54 factors family, score 42.30, E-value 8.4e-20"	
1489..2739	gene
/gene="rpon"	
1489..2739	CDS
/gene="rpon"	

```
/note="Cj0670, rpoN, probable RNA polymerase sigma-54 factor, len 416 aa; similar to many e.g. RP54_BACSU RNA polymerase sigma-54 factor (436 aa), fasta scores; opt: 357 z-score: 603.0 E(): 2.7e-26, 28.9% identity in 443 aa overlap, and RP54_ECOLI (477 aa), fasta scores; opt: 365 z-score: 483.2 E(): 1.3e-19, 28.8% identity in 459 aa overlap, 47.4% identity to HP0714. Contains PS00718 Sigma-54 factors family signature 2, Pfam match to entry PF00309 Sigma54_factors, and helix-turn-helix motif at aa 303-324 (score 1227; +3.37 SD)"/codon_start=1/transl_table=11/product="RNA polymerase sigma-54 factor"/protein_id="CA872947.1"/db_xref="GI:6968132"/translation="MLKQITQAPKTKISQTRSLWPLIQANIEDLKENLDFARNPFLNVDISQTHDKGNFYDFYKHVNSAFYSDVSKLAKSVYELNEQLPLPFTSKSOLEAKITCEDNEGYFHEDEFLKEYSLIEIRVRFKFLDGVGKDYKEAFLFALENMELDEIDECFLMIDFNIQNTYKPELVKALVKLRSTPFLPYFEDSRITVPDIFYKENGELKVKLINDDYYPEISITQDGLHDFLSHYIKKAKNLVLAWRKATLYKIGLIVEXQYDFFMGKEIKPMFTFDLALDLERNASTISRAVANKYLSCEGLIPLKDFAFALDEGSEISVNGVKEFVANLVKNEDRNPLSDSKILEIKKEFKVDIGRRTITKYRKHNLNIASTDRKKLYELEG"2656..2679/gene="rpoN"/note="PS00718 Sigma-54 factors family signature 2"2903..4327/gene="dcuB"2903..4327/gene="dcuB"/note="Cj0671, dcuB, probable anaerobic C4-dicarboxylate transporter, len: 474 aa; highly similar to e.g. DCUB_ECOLI anaerobic C4-dicarboxylate transporter (446 aa)/opt: 1280 z-score: 2918.6 E(): 0, 69.1% identity in 466 aa overlap. No Hp ortholog. Also similar to Cj0088, dcuA (37.0% identity in 465 aa overlap)"/codon_start=1/transl_table=11/product="putative anaerobic C4-dicarboxylate transporter"/protein_id="CA872948.1"/db_xref="GI:6968133"/translation="MDFLTSLSAEGQFAIQIIVILICLYGAKKGIGIALGLGGIGILMLVFAPHKPGKPAIDVMLTILAVVAVGATLQASGLDVMQIAERILRRNPKELTILAPFVCFITLCGTGHVVTIMPIIVYDAIKNGIRPERMVAAISISOMGIITASPVAVSITALLNNAHKLAGEGQYINLQITPSTLFGVLCIGIFSFRGKDKDQVFOEKLDPKEPKYVGSQILLGVKLPKSNVAMWIFLGAIALVALLGVDFDLRWNGQVXKNGIPQVDALGNKMDLVMSVSIOMELLAGSLIIFTKTDARKIGSNEIFKSGMIALVAVFGISWADMTFVHTPMKKAALGDIVKEHPWTYAVMLLLSKFVNSQAAISA FVPLALGIVGEPGVTAFAAACYGYYILPTVPSDLATIQFDRSGTHIGKFVNHSTI LPGLIGVITSCIAGYFIAMAAGYL"4469..4657/gene="Cj0672"4469..4657/gene="Cj0672"/note="Cj0672, possible periplasmic protein, len: 62 aa; no Hp match. Contains possible N-terminal signal sequence and second hydrophobic domain"/codon_start=1/transl_table=11/product="putative periplasmic protein"/protein_id="CA872949.1"/db_xref="GI:6968134"/translation="NRKQSPMDIIFALLLLLLAFGLSCFFICFCEIQTKDTRNIFLLVL SLILALYFIALLYPERK"4667..4810/gene="kdpA"4667..4810/gene="kdpA"/EC_number="3.6.1.36"/note="Cj0676, kdpA, probable potassium-transporting ATPase A chain pseudogene, len: 1744 bp; highly similar to e.g. ATKA_ECOLI potassium-transporting ATPase A chain (EC 3.6.1.36) (557 aa). No hp match. Note they kdpC (Cj0677)
```

```
is intact, while kdpC (Cj0678) is a pseudogene"/codon_start=1/pseudo/transl_table=11/product="pseudogene (potassium-transporting ATPase A chain)"/5521..5529/note="g(9)"/gene="kdpB"6371..8416/gene="kdpB"6371..8416/gene="kdpB"/EC_number="3.6.1.36"/note="Cj0677, kdpB, probable potassium-transporting ATPase B chain, len: 681 aa; similar to e.g. ATKB_ECOLI potassium-transporting ATPase B chain (EC 3.6.1.36) (682 aa), fasta scores; opt: 2419 z-score: 2798.9 E(): 0, 56.6% identity in 678 aa overlap. No Hp match. Contains PS00154 E1-E2 ATPases phosphorylation site and Pfam match to entry PF00122 E1-E2_ATPase. Note that kdpA (Cj0676) and kdpC (Cj0678) are pseudogenes"/codon_start=1Query Match 2.7%; Score 140.6; DB 2; Length 317511; Best Local Similarity 49.0%; Pred. No. 1e-08; Matches 557; Conservative 0; Mismatches 559; Indels 21; Gaps 6;QY 1093 tattatacaaaatcggtggaactgatgccagtaggatactctctgattagcacatttt 1152Db 134900 TTTTATTAAGTGGGTTCAAGAAATGAGATCATGGGAAAAAGTGCATATGT 134959QY 1153 ttgaacacttaatttagtgaacagaaaaatt-----tctaatctcatcagcac 1206Db 134960 TGAACATTTAAATTTTAAAGTACTTAAAAATTTAAAGCTGGCGAATTTGATGAGATTG 135019QY 1207 ttagtaataatagcggaatttcaatgcaagcacatctcaattttgtactatactacg 1266Db 135020 TTAAGGTTTGGTGGTGATATGCAAGCACAGGTTTGACTATATCTATTATA 135079QY 1267 aattaataccaaaacaattatttatctctgcaatggaattgaatcagacagaatgcaga 1326Db 135080 TTAATGTGCGAAGAAAAATTTAGATAAAGCTTTAGAGCTTTTTCGACAACTATATGGCA 135139QY 1327 atttlaaggtttaccacaaagcattaataagagaacaaagtagctcttagaagaagaa 1386Db 135140 ATTTAAATTTAAAGATGAGAAATTTACCCCTGAAGAGCAGCTGGTTTGAAGAGCCGTA 135199QY 1387 aaatgag---agttgaagcccaagcaaaaaacatactagaagaagaaatggaaaatgcat 1443Db 135200 GATGGAGAACAGATAATAACCCCTTAGGATATCTTTATTTTAGGCTTTTAAATCATGCAT 135259QY 1444 ttattacaatggatattggcagaccagtagtaggtaggatgggaacatgaattagcaactaca 1503Db 135260 TTATGTATCATCTTATCATTTGGACTCTCTATAGGTTTTTTTAAAGGATATAGAAAAATTGGA 135319QY 1504 acaagaagtgtcgaagcctttcataagctacattatagtccttaataatgctatataa 1563Db 135320 GTATTGAAGATATTAAAGAAATTTACAGTATTATTATCAACCTAAAATGCGATTTTAC 135379QY 1564 ttgttaactggagatcagatccacagaagtaatacacacttgcaaaaaataactatg99ga 1623Db 135380 TTGTAAGTGGCGATATAGAAAGTAAGGAAGTTTTTGGAGCTTTCAAAAAAACATTTTGAAA 135439QY 1624 aaataccatcctaataagaacaccttcaagtcaggtagagtaggtagaaccacccgcataaaa 1683Db 135440 AGATTTAAAAATTAAGACTATACCTAAAATTTACACAAAAAGAGCCTTAAGCAAGATTGAG 135499QY 1684 caaatatgactttaacattaaagacagttcagtagaatacccaagaactgttttaagt 1743Db 135500 TAAAAAGAAATATTATTACATAAAAACTCAGATACCTGAAGTACTATTAGCCCTTGCCT-----T 135553QY 1744 atcaaatcaccaaatggattaccataaaaaactacatacttaacatgatgttagcagaaa 1803
```

Db 135554	ATAAATTCCAAATTCA--AGCACAAGATATACCTGCTTTAAATGCT-TTATCGGACC	135610	MEDLINE
Qy 1804	tactcgtagtgtaaaattcagcctgcttcaaatgattggtgaattacaatcaatag	1863	REFERENCE
Db 135611	TTTTAGGAAGTGGGAAAGTCTTTAATGAGTGAAATTTTGATTGATTAATTAATTTAA	135670	TITLE
Qy 1864	ttatcgcgataaaacagagatttaattacttaactgacgcgataattacccttcattg	1923	JOURNAL
Db 135671	TCAATGATTATTGCTTATGTTAATGATTGATTATAGAT---GAAATTTATTATTATTTA	135727	MEDLINE
Qy 1924	aagctatactaaaacgggattctacagaagcgttagaacaagaataatcataatgta	1983	REFERENCE
Db 135728	TTTGTAATGTGAACCCCAATGTTAATGCAAAAAGTAGAAAAGAGCTTTTAAATAATCA	135787	TITLE
Qy 1984	taaaataattattagaataatcagcagataatttagaagaagcaagatataaag	2043	JOURNAL
Db 135788	TTGATAAACTTAAATGGGTAAATTTCTCAAAAGATTTCGAAGAGTGAAATAATAG	135847	MEDLINE
Qy 2044	taaaagcaatttaacttatgattgacggactaaccttcatactatattttatgga	2103	REFERENCE
Db 135848	TCAAAAGTGATTTTATTTCTCACTTAACAATGCTAGTCAGTGGCAATATTTATGTT	135907	TITLE
Qy 2104	tcacatctaactagagtagcgcgtatcagaatacagtaattttacagataccatagaca	2163	JOURNAL
Db 135908	CATATCTACAGAGAGATATCAATCTTTGTTAAATTATGAGAAAGATATACAAAATT	135967	MEDLINE
Qy 2164	aagtgaattccaagattgtaactcgcgtatggaataatctttcaaaacaataaa	2220	REFERENCE
Db 135968	TGGAATTAAGATTGATTCTTCTGCTTAAATAATTTTATTCAGAAATTCNA	136024	TITLE
RESULT 6			SOURCE
DMU37541	19517 bp DNA circular INV 04-APR-2000		ORGANISM
LOCUS	Drosophila melanogaster complete mitochondrial genome.		
DEFINITION	U37541		
ACCESSION	U37541.1		
VERSION	GI:1166529		
KEYWORDS	Drosophila melanogaster.		
SOURCE	Mitochondrion Drosophila melanogaster		
ORGANISM	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
REFERENCE	1 (bases 12511 to 12682)		
AUTHORS	Clary,D.O., Goddard,J.M., Martin,S.C., Fauron,C.M. and Wolstenholme,D.R.		
TITLE	Drosophila mitochondrial DNA: a novel gene order		
JOURNAL	Nucleic Acids Res. 10 (21), 6619-6637 (1982)		
MEDLINE	83090428		
REFERENCE	2 (bases 5269 to 5695)		
AUTHORS	Clary,D.O., Wahleithner,J.A. and Wolstenholme,D.R.		
TITLE	Transfer RNA genes in Drosophila mitochondrial DNA: related 5' flanking sequences and comparisons to mammalian mitochondrial genes		
JOURNAL	Nucleic Acids Res. 11 (8), 2411-2425 (1983)		
MEDLINE	83220794		
REFERENCE	3 (bases 404 to 5272)		
AUTHORS	de Bruijn,M.H.		
TITLE	Drosophila melanogaster mitochondrial DNA, a novel organization and genetic code		
JOURNAL	Nature 304 (5923), 234-241 (1983)		
MEDLINE	83245048		
REFERENCE	4 (bases 804 to 1778)		
AUTHORS	Satta,Y., Ishiwa,H. and Chigusa,S.I.		
TITLE	Analysis of nucleotide substitutions of mitochondrial DNAs in Drosophila melanogaster and its sibling species		
JOURNAL	Mol. Biol. Evol. 4 (6), 638-650 (1987)		
MEDLINE	88174373		
REFERENCE	5 (bases 5268 to 13619)		
AUTHORS	Garesse,R.		
TITLE	Drosophila melanogaster mitochondrial DNA: gene organization and evolutionary considerations		
JOURNAL	Genetics 118 (4), 649-663 (1988)		
88212147			
6 (bases 441 to 2967)			
Satta,Y. and Takahata,N.			
Evolution of Drosophila mitochondrial DNA and the history of the melanogaster subgroup			
Proc. Natl. Acad. Sci. U.S.A. 87 (24), 9558-9562 (1990)			
91088557			
7 (bases 14215 to 14512)			
Ballard,J.W., Olsen,G.J., Faith,D.P., Odgers,W.A., Rowell,D.M. and Atkinson,P.W.			
Evidence from 12S ribosomal RNA sequences that onychophorans are modified arthropods			
Science 258 (5086), 1345-1348 (1992)			
93088057			
8 (bases 14917 to 19517)			
Lewis,D.L., Farr,C.L., Farquhar,A.L. and Kaguni,L.S.			
Sequence, organization, and evolution of the A+T region of Drosophila melanogaster mitochondrial DNA			
Mol. Biol. Evol. 11 (3), 523-538 (1994)			
94285822			
9 (bases 1 to 408; 13319 to 19517)			
Lewis,D.L., Farr,C.L. and Kaguni,L.S.			
Drosophila melanogaster mitochondrial DNA: completion of the nucleotide sequence and evolutionary comparisons			
Insect Mol. Biol. 4 (4), 263-278 (1995)			
96423163			
10 (bases 1 to 19517)			
Lewis,D.L., Farr,C.L. and Kaguni,L.S.			
Direct Submission			
Submitted (03-OCT-1995) Laurie S. Kaguni, Biochemistry Department, Michigan State University, East Lansing, MI 48824-1319, USA			
Location/Qualifiers			
1. 19517			
/organism="Drosophila melanogaster"			
/organelle="mitochondrion"			
/db_xref="taxon:7227"			
/note="derived from new and previously submitted sequences; sequence is a composite containing sequences obtained from different Drosophila melanogaster strains"			
1. 65			
/product="tRNA-Ile"			
complement(97. 165)			
/product="tRNA-Gln"			
171. 239			
/product="tRNA-Phe"			
240. 1265			
/codon_start=1			
/transl_table=5			
/product="NADH dehydrogenase subunit 2"			
/protein_id="AAC47811.1"			
/db_xref="GI:1166530"			
/translation="MFNNSKILFTTITMIGTLITVTSNWLGAWMGLEINLLSPFL LSDNNLMSTEASLYKVELTOVLASTVLLFSSILLMLKNNMNEINSEFTSMISALL LKSNAPHFHFEPNMEGLTWMNALMTWKIAPLMILSYLNIKYLILLVILLSVII GAIGLNQTSUKRLMAFSSINHLGMLSSMISEWILFFSFLSFVLTFFMNFIF KLFLNQLFSWFVNSKILKTLFNMFLSLGGLPPFLGFLPKVLVTOQLTNCQFMFLT IMMSTLTTLFFYLIRICYSAFMNYFENNWKMMNSINMYMIMTFFSIFGLFLI SLFFVFMF"			
1264. 1329			
/product="tRNA-Trp"			
complement(1322. 1383)			
/product="tRNA-Cys"			
complement(1403. 1468)			
/product="tRNA-Tyr"			
join(1470. 1472,1474. 3009)			
/codon_start=1			
/exception="mechanism underlying reading frame shift after first codon uncertain"			
/transl_table=5			
/product="cytochrome c oxidase subunit I"			
/protein_id="AAC47812.2"			
/db_xref="GI:7412849"			
/translation="MSRWLFSTNHKIDGTIGTYFIFGAWGMVGTSLSLIRAEHLHPG			

```
trNA      /product="trNA-Leu"
CDS       /note="TAA stop codon is completed by the addition of 3' A
          residues to the mRNA"
          /codon_start=1
          /transl_except=(pos:3767,aa:TERM)
          /transl_table=5
          /product="cytochrome c oxidase subunit II"
          /protein_id="AAC47813.1"
          /db_xref="GI:1166532"
          /translations="MSTWANGLQDSAPLMEOLIFPHDHALLILVMTIVLGVLMFM
LFNNVYNRFLHQLQIEMLWTILPALILLFIALPSLRLLYLDEINEPSVILKSIGH
QWYSYEIDFNIEFSDSYMIPNELMDGFLDDVDNRVLPNMQSIRLLVTAADV
HSTVPALGVKVDGTPQLNQTNFFINRPLGFLYGCQSEICGANHSFPIVIESVPVNY
FIKWSNNNS"
          3768..3838
          /product="trNA-Lys"
          3840..3906
          /product="trNA-Asp"
          3907..4068
          /codon_start=1
          /transl_table=5
          /product="ATPase 8"
          /protein_id="AAC47814.1"
          /db_xref="GI:1166533"
          /translation="MPQMAPISWLLLIIFSIITFLFCSINYSYMPNPKSNELKNI
NLNSMNWKN"
          4062..4736
          /codon_start=1
          /transl_table=5
          /product="ATPase 6"
          /protein_id="AAC47815.1"
          /db_xref="GI:1166534"
          /translations="MNTNFSVFDPLAIFNFSNLWLSFLGLLMPISYIWMPSRYNI
MWSILLTLHKPEKTLGPSGHNGSTFIFLSFLILFNNFMGLFVPIFTSTSHLPLT
LSALPLNLCFMLYGHNIHQHMFALHPGCTPAILMPNVCJETISNIIRPGLAVR
LTANMIAGHLLLLGLNGTSSSYMLMTFLMQAIIALLVLESAMVMIQSYVFAVLSTL
YSSEVN"
          4736..5524
          /codon_start=1
          /transl_table=5
          /product="cytochrome c oxidase subunit III"
          /protein_id="AAC47816.1"
          /db_xref="GI:1166535"
          /translations="MSTHSNHPHFLVDYSWPLTGAIGMTTVSGMKWKFHOYDISLF
VLGNIITLTVQWRDVSREGYQGLHTVAVTIGLRWGMILFILSEVLFFVFFVFAF
FHSLSPAIFELGASWPMGIIISFNPEQIPLLNTAIIILASGVTVTWAHSLMNNHSOT
TQGLFTVLGIIYFTIIOAYEIEAPFTINDSIYGTFFFNATGFGHGHVLIIGTFLLV
5543..5607
          /product="trNA-Gly"
          5608..5961
          /codon_start=1
          /transl_table=5
          /product="NADH dehydrogenase subunit 3"
          /protein_id="AAC47817.1"
          /db_xref="GI:1166536"
          /translations="MFSIIFALLIILLITIVMFLASILSKKALIDREKSSPPECQFD
PKSSRLPFSLRFLITILIFIDVEITALILPMIIMKYSNIMWIITSIIFILILI
GLYHKNQGLMNSN"
          5981..6045
          /product="trNA-Ala"
          6055..6118
```

```
trNA      /product="trNA-Arg"
          6119..6183
          /product="trNA-Asn"
          6184..6251
          /product="trNA-Ser"
          6252..6318
          /product="trNA-Glu"
          complement(6337..6401)
          /product="trNA-Phe"
          complement(6401..8124)
          /note="TAA stop codon is completed by the addition of 3' A
          residue to the mRNA"
          /codon_start=1
          /transl_except=(pos:complement(6401..6402),aa:TERM)

Query Match      2.6%; Score 138.2; DB 33; Length 19517;
Best Local Similarity 42.9%; Pred. No. 4.3e-08;
Matches 1541; Conservative 0; Mismatches 1988; Indels 60; Gaps 15;

Qy 490 taaactcatcactcttctcatgtatcttcttaagtacaaagaataaacttcataccg 549
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 14781 TAAATTTCTTTAATTAATATATTAATTAATCTGCAATAAATTTTCATATTTATTTTAA 14840
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 550 tacattaaactgattaaaaaaataaacttaattgagcaaaaataatttatctatt 609
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 14841 ATAAATATAAAATCACACAAAAATTTACATATAAATCAAAATTAATAACAAAAATTTTAAAGC 14900
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 610 caacagattctttcaattagagagtattcaaaaacactcaactactgcttgcaacttt 669
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 14901 CAAAATAAACTTTAAAT-----TTTATTTTGTATTTTATTTATTAATAATAA 14948
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 670 ctatcactgatatataaagtgaaataaatttaaaaacttttagtttaataagagaatt 729
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 14949 ATATTATAATTTTATAAAATAAATTTTAAAGAAATAATTAATAATTAATTTAATAA 15008
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 730 ttattaaaactgttgatcaaatttaattactgatataaaaaataactattataaataa 789
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 15009 ATATTAAATAAATTAATTTTATAATAAATTTTATCATATTAATAAT--AATATAAAAA 15066
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 790 atgcttaataagattattattaccttaattcacttaacttaacaccttaacaaattcata 849
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 15067 TTTTATAAATTTATTTTAAATTTTACAAAATTTTAAATAATTTTATTTTATTTTAAAAAA 15126
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 850 ataaaaatacttactcttatttttttacccttgatattattataataatcataaaact 909
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 15127 AAATAATTTTACAAAAAAATAATTTATCAAAATTAATAATAATAATAATAATTTTAATT 15186
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 910 cccaaataaactattgcaaggttatggaatgatgaaatttttttacttggtttttctatag 969
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 15187 TTAATAATAAAAATTTTAATTTTACACTTTTAAAAAATATTTTAAAAAATAATTTTAAAAAATAAT 15246
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 970 tttcttaacaatagccaatcatgcttttctcttaacatttaacaggttacacagaaaaat 1029
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 15247 TTTTAAAAAATAAATAATTTTAAAAAATAATTTTAAAAAATAATTTAGATTTAATT 15303
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1030 tagataatggaatggaatgattcccaatcatcgccaccagcagtcagtcacaca 1089
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 15304 TCITTTAAATGACTAAAAAATAATTTTAAAGTATTTTAAAGTATTTTAAACATTTTAAAAAATAAT 15363
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1090 tggattatacaagtcggtggaactgatccagtaggatactctggtattagcacatt 1149
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 15364 TTTTAAAAAATAATATAATAATAAATAATTTTAAAAAATAATTTTAAAAAATAATGAAA 15423
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1150 ttttgaacacttaattgttagtggacacagaaaaatttctctatctcagcacatta 1209
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 15424 ATATATATAAATAATAATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 15483
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1210 gtaataagcggaaatttcaatgcaagcacatctcaattttgtactatactacgaat 1269
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 15484 ATTA-AAATTTTATGAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 15542
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1270 taataccaaacaatatattctctcttgcaatggatattgaatcagacagagaatgcagaaat 1329
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
```

Db 15543 ATATAATAAATATTCGATTATTAATAATAATTAACGAATAATAATAATAATAATAATAA-T 15601
QY 1330 ttaagggtaccgacaagcatttaataagagacaacaaaggtagctttagaagaagaagaaaa 1389
Db 15602 TTATTTTAATCACAATCTGAATTAATTAATATATATATATATATATATATATATATACA 15661
QY 1390 tgagagtgtaagccaaagcaaaaacatactacgaagaagaagaaatggaaaaatgcattttatt 1449
Db 15662 TATATATATATATATACATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 15721
QY 1450 acaatggatagcgacacagtagtaggagtggaacatgaatgaatagcaacatacaacaag 1509
Db 15722 TTATTTATTAATTAATAAATCTTAAAGATTTATTTTAAAGAAAAATTTATTTATTAATTT 15781
QY 1510 aagttgctgaagccttcaaaagctacattatagctcctaataatgctatataatgaatga 1569
Db 15782 ATACTTAATAAATCTATTTTATTAATAAATTTATTTATAATAAATAAATAAATAAAT 15841
QY 1570 ctggagatgcagatccacaagaagtagatcacacttgcaaacataactatg9gaaaaatc 1529
Db 15842 AATAAGAAATATTTTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 15901
QY 1630 catctaataagaacacctcaagctcaagcttagggtagaacaccgcgataaaacaata 1689
Db 15902 ATTTATATATATATATATATA-TAATTTTAATTTTCAATTAATTAATAATAATAA 15959
QY 1690 tgactttaacatlaaaagacagttcagtagaatacccagacgtttttaaagtatcaaa 1749
Db 15960 TAAATAATTTTATTTAATCACATAATCTGAATAATTAATTAATAATAATAATAATA 16019
QY 1750 taccaaatggtataccaataaaactacatacttaacatgagtgttagcgaaataactcg 1809
Db 16020 ATAAAAAAATGAAATAAATTTATTCCTCCCTATTCATAAATTTATTTGTATAAATAA 16079
QY 1810 gtagtgttaattcagcctgtcttacaatgattgttgtaataacaatccaatgattacat 1869
Db 16080 TAAAAAATATTTTATTTTAAAAAATAATGATTTTAAATAATTAATAAATAATTTTAA 16139
QY 1870 cgataaaacagattataacttaactgaactgacagcgataatt-----accttccattg 1923
Db 16140 TTATAATAAATTTTATTAATAAATAATTTTAAATAATTAATAAATAATTTTAAAT 16199
QY 1924 aegcttacctaaacagggatctctacagaagctgtagacaagaatactcaaatgta 1983
Db 16200 ATATAAATAATTTAAAAATGATTTTATAAATAATTTCAATTCATATATTTATATATATA 16259
QY 1984 taataatatttagaaaaatggaaatttcagcagaataatttagaaagtgcaagtataaag 2043
Db 16260 CATATAATTTTAAATTTCAATTAATAATTTATTAAGTATAATAAATAAATAATTTTAA 16319
QY 2044 taagaagcacatttaacttatgcat-ttgacggactaacttccatcatcatattttatggc 2102
Db 16320 TAAATCTGAATTAATTTGTATATATATATATATATATATATATATATATATATATAT 16379
QY 2103 atgcataactagtaggtagccgtctatcgagaatcagtaataattttacgataccatagac 2162
Db 16380 AATTTATTCCTCCCTATTCATAAATTTATTTATATAAATAAATAAATAAATAAATAAAT 16439
QY 2163 aaagtgaagtccaagatgtaactccgcgtatggaaaaatactttcaaaaacaataaaga 2222
Db 16440 TAAAAAATAAATTTATTTTAAATTTTACTTAAATAAATAAATAAATAAATAAATAAAT 16499
QY 2223 ttaacgggcatatttacctaagtaggaatagttatgagaacaatattgtgtacacat 2282
Db 16500 ATAAATAAATAATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 16554
QY 2283 taattattgattttcttttccattccaatcacatgcaaat-----gactccaatat 2331
Db 16555 TAAAAATAATTTTAAAAAATTTCAATTTATTTATATATATATATATATATATATATAT 16614
QY 2332 taacataaagaagctacaactaaaaataaaaaatacactatctatattgttgaaacataaa 2391
Db 16615 AATTTTCAATTAATTAATAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 16674

QY 2392 cctaccacaacatttcccttaaaatttgcattccaagaagcagagatacgccttatgatgcctt 2451
Db 16675 ATAATTAATTAATTAATATATATATATATATATATATATATATATATATATATATATAT 16734
QY 2452 tgataagcagagacttgcactactttacatacaaaaaattataacgaaggatcaaaaaacaa 2511
Db 16735 TTCCATAAATTTATTTGTATATTAATTAATAAATCTTAAATAAATTTATTTTAAAAAATA 16794
QY 2512 ctatgctccagtttgcacaacaattagaaggcaaggtat----agacttaaaatttg 2567
Db 16795 TTATTAATAATTAATTAATTAATAAATCTTATTTTAAATAAATTTTATTAATAAATAAAT 16854
QY 2568 atatagcactagacaatttttatatatcatcttaaaaccccttcatagaaaaacctttgaaga 2627
Db 16855 TTAATAATAATTAATAAATAATTTTAAATAATAATAAATAAATAAATAAATAAATAAAT 16914
QY 2628 cccatgtttactcagtgatgcatattcaaacccgctcacagatcaagaataattcaata 2687
Db 16915 ATTCAATTCATATATTTATATATATATATATATATATATATATATATATATATAT 16974
QY 2688 gaataatagcagaacagattgcacatgttaaatcattatatctgctccctgaatttatag 2747
Db 16975 GTATAATAAATAAATTTATTTTAACTCAATAATCTGAATAATTAATTTGTATATATAT 17034
QY 2748 ctacaacagaatgaatcacgcttatattcaaaagggcaccccatattctcaaaaagtttaag 2807
Db 17035 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 17094
QY 2808 ggacattaaatacaacaataataatacaaccaggaagaagcttgc-----attatatata 2860
Db 17095 TAAATTAATACTTAAAAAATAATTTTAAAAAATAAATAAATAAATAAATAAATAAATA 17154
QY 2861 aaaaaatgctttgacagaaggaacaaatcgttatcagcgagcagagagatgtagatccaaca 2920
Db 17155 ATAACTATTTTATTAATAAATAATTTTATTAATAAATAAATAAATAAATAAATAAATA 17214
QY 2921 cagctacaaatttactagataaataattcttccaaattgccaatcctggttaataacaaa 2980
Db 17215 ATTATATATATATATATATATATATATATATATATATATATATATATATATATATAT 17274
QY 2981 aatacaccacccagatcagcactgttaatagagaagacacattatttatgtacagagagat 3040
Db 17275 AATAAATAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 17334
QY 3041 gtaccacaagtgctcaaatgttctgctacagacacagtagaccatacatcacagcaagcact 3100
Db 17335 TAAATAAATTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 17394
QY 3101 catgcatcaaaccttgttcaactactatgtagcggaattgaagctcactcaattcaattaaatg 3160
Db 17395 AATAAATAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 17454
QY 3161 atagaatttaagagacaagtttaggattaaacataccacagtagcaggttccactatccaacatg 3220
Db 17455 ATAAATTTTATATATTTATGAATATTTATATATATATATATATATATATATATATATAT 17514
QY 3221 aatca-tagtaagtgtctatttgggtacaataattcactgataataccacagtaacaaatg 3279
Db 17515 TTTAAATAAATTTAATAAATAAATTTTAAATAAATTTCTTAAATGTATTTATTTTATATA 17574
QY 3280 tatatccgtcttcaacagatattatagagcacattcaaaaagtaggggtgtgtagaagcac 3339
Db 17575 TATTTATATAATAAATCATGTITTTTAAAAAATAAACAATAAATAAATAAATAAATAAAT 17634
QY 3340 ttttgaattgcaaaatcagtagtattaccacactcttttttttttctctatgttgaatacaaa 3399
Db 17635 TTTTAAATGAATAATAATTTATTTTATTTTATTTTATTTTAAAAAATAAATAAATAAATA 17694
QY 3400 taatgtagtagagatattgttaagcttacaattcacagatctagatcccgaggttatataa 3459
Db 17695 TAAATTTTTTTTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 17754

KEYWORDS HTG: HTGS_PHASE1.
SOURCE malaria parasite p. falciparum.
ORGANISM Plasmodium falciparum
REFERENCE 1 (bases 1 to 163226)
AUTHORS Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
Kurtz, R.W., Fung, E.L., Qin, F., Rowley, D., Mao, J., Tamaki, T.,
Kurtz, O.B., Conway, A.B. and Davis, R.W.
TITLE Plasmodium falciparum 3D7 chromosome 12
JOURNAL Unpublished
JOURNAL 2 (bases 1 to 163226)
AUTHORS Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W.
TITLE Direct Submission
JOURNAL Submitted (19-FEB-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto, CA
94304, USA
On Jun 29, 2000 this sequence version replaced gi:7243830.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 5541: contig of 5541 bp in length
* 5542 5741: gap of unknown length
* 5742 72759: contig of 67018 bp in length
* 72760 72959: gap of unknown length
* 72960 88038: contig of 15079 bp in length
* 88039 88239: gap of unknown length
* 88239 163226: contig of 74988 bp in length.
FEATURES
Location/Qualifiers
1..163226
/organism="Plasmodium falciparum"
/db_xref="taxon:5833"
/chromosome="12"
/clone="PFYAC293"
/clone="307"
BASE COUNT 65620 a 14825 c 14808 g 67373 t 600 others
ORIGIN
Query Match 2.6%; Score 136.2; DB 68; Length 163226;
Best Local Similarity 43.6%; Pred. No. 4.1e-08;
Matches 1048; Conservative 0; Mismatches 1338; Indels 19; Gaps 9;
Qy 1833 tacaatgattggttaatacaatccaatagcttaccatcgataaaacagagataataatc 1892
Db 106740 TATAATATATATTTTAAATTTATATAAATAAATAAATAAATAAATAAATAA 106681
Qy 1893 ttaactgacagcgaataattacccttccattgaagctacacataaaacggatctctaca 1952
Db 106680 ATATCAAAATTAATCATTTATTAATTTATTAATATATTAATTAATTAATTAAT 106621
Qy 1953 gaagctgtagacaagaattcaataatgataataattatttagaataatggaattcca 2012
Db 106620 TTAATAAATTAATAGTTAATTTATTAATAAATAAATAAATAAATAAATAAATA 106561
Qy 2013 gcagaatatttagaagtcgaagataaagataaagacacatttaactatgacattgac 2072
Db 106550 TATAAATTAATTCATATACACATTAATTAATAAATAATGAATTAATTAATAAATA 106501
Qy 2073 ggactaaccttccatcatatttttggcattgcacatcaactagcaggtacccgctatca 2132
Db 106500 ATAGAAAAATTAATACAAATTTAATTAATTAATAAATAAATAAATAAATAAATA 106441
Qy 2133 gaaatcagtaattattcagataccatagacaaagtaagatccaagatgtaactccgct 2192
Db 106440 AATAAATAATTAATTAATTAATTAATAAATAAATAAATAAATAAATAAATAAATA 106381
Qy 2193 atggaataatcttccaacaataatagattaaacccggcattttattccatcaatgagaa 2252
Db 106380 AATATAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 106321

Qy 2253 tagttatgagaa---acatatgtgtgttacacattaatattgattttcttttccattcaata 2309
Db 106320 ATTTTAATTAATAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 106261
Qy 2310 catatgcaaatgctcaatattataacataaaagaactcaacataaaataaataacact 2369
Db 106260 AATTAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 106201
Qy 2370 atctatatgttgaaacatcataacctaccacaaatttcccttaaaatttgcttcaagaag 2429
Db 106200 AATAATATATATTAACAAATTAATTAATTAATAAATAAATAAATAAATAAATAAATA 106141
Qy 2430 caggatcacgcttattgctccttgataagcaaggacttgcatactttacatcaaaaatat 2489
Db 106140 AATTAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 106081
Qy 2490 ---taaacgagatcaaaaaaacacactatgctctcagtttgcacacaattagaagcga 2546
Db 106080 ATATATTTAGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 106021
Qy 2547 aaggtatagacttaaaatttgatagacctagacacacacatttttatatat-----cattaaa 2601
Db 106020 TAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 105961
Qy 2602 aacctatcacgaaacactttgaagaagccctagtttttactcagtgattgcataatcaaac 2661
Db 105960 TATATATACAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 105901
Qy 2662 cgtcacgatacaagaataatcctaagataaataagacagacagattgcacattgaaatc 2721
Db 105900 AAATATATATATATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 105841
Qy 2722 attatatctgctcctgaattttagctacacagaaatgaatcacgcttatattcaaaag 2781
Db 105840 ATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 105781
Qy 2782 gcaccatatttcaacaaagtttacgggacattaaatacaaatcaa---taataatcaaacag 2839
Db 105780 TAAATTTATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 105721
Qy 2840 gaagacgttcattatataaaaaatagttttgacaggaacaaatcggtatcagcgca 2899
Db 105720 TAATATATAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 105661
Qy 2900 gcaggagatgt-agaatccacacagctatcaaaatttactagataaaatattcttccaa 2958
Db 105660 TAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 105601
Qy 2959 attgccatctggtaatacaaaaaataccataccagatacagactgttaatagagaagcac 3018
Db 105600 ATATTAAACAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 105541
Qy 3019 attattatgtacagagagatgtaccacaaagtgctcataatgtttgctacagacacagt 3078
Db 105540 ATAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 105481
Qy 3079 accatatcacagcaaaactatcatcatcaaacctgttcaactactatgctagcgagatt 3138
Db 105480 ATAATGTTTTTATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 105421
Qy 3139 aagtcctcaattcaattatgataagataagagacaaagtaggattagattacacattag 3198
Db 105420 AAG--TTAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 105363
Qy 3199 tagcagttcactcaatcaatgaatcatagtaagtctgcttattggtacaaattattcaactga 3258
Db 105362 TATATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 105303
Qy 3259 taataccacagtaacaaaatgtatccgtcttaacagataattatagagacacataaaaa 3318
Db 105302 AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 105243

QY	3319	gtatgagtgatgaagacacattttgc-aattgcaaatctagattacacaactcttta	3377
Db	105242	TTATTATAATAAATACATAAAATATTTATTACTATATATTTAAATAAATAAGTATA	105183
QY	3378	ttttatctatgttaaataacaataaagttagtgagatattgttaagcttacaattacacg	3437
Db	105182	AAATTATCTTCTTAATTTATATTTTAAATTAATTAATATATATATATAATTTATAA	105123
QY	3438	atctagatcgcaggttattataataacatactcttactacaagaacaatacaatgaag	3497
Db	105122	ATAAATATATTTTATTTTAAATTAATTAATTAATTAATTTATTTGTTTAAAT	105063
QY	3498	aagtaataaaatgcacgaagaattttatctaatgaatagtaataaagtaggagaa	3557
Db	105062	ATTTAATCTACTATAATATATTTAATTAATTAATTAATTAATTTATTTT	105004
QY	3558	aaacaataacataaaatggcaacaataagatgctcaaaaacacacacctgttgaagta	3617
Db	105003	AAATAAAATAATATATTAATAAATGAATAAATAAATAAATAAATAAATAAATAA	104944
QY	3618	tacaggttatgttattactacaagattctctattagttgattaagtaagtaagtag	3677
Db	104943	TATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTAAATTA	104884
QY	3678	cttcaatcaataaaaaaacattacaacaagtggttagctctaccgagagaagcttata	3737
Db	104883	TAATGTTTATTTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAA	104824
QY	3738	agcttttaacctgggaataataagaagtttgcataagttgaagcaaaaaattagtaacac	3797
Db	104823	AATTAATAAATAAATAAATGAATTAATTTATTTTAAATAAATAAATAAATAAAT	104764
QY	3798	aatatcaaaattttctacaggatttatattgtgacctaccatacaacctatttagaa	3857
Db	104763	AATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	104704
QY	3858	aatgaacaacagatacacacatcaataaattatcactacaattccaattataaacaatga	3917
Db	104703	TATATAATAAATAAATAATTAATTTATTTTAAATAAATAAATAAATAAATAA	104644
QY	3918	gtatttttacttaattatttaattttatttttttaaaataaaataatttacttactc	3977
Db	104643	TTTAATTAATAAATAAATAATATATAATAAATAAATAAATAAATAAATAAATAA	104584
QY	3978	aataaagcagttactaccagtagtattggtgatttaagtcgagcaattactactaa	4037
Db	104583	TTAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	104524
QY	4038	tagtatagctgttgacaagccgcaatctgcggttcttgacaaaataataactaatcagta	4097
Db	104523	TTTATTTTATTTTATTTTAAATTAATTAATTAATTTATTTTATTTTAAATAAATAA	104464
QY	4098	aaattttgaagtggttcaccataatggtgatta-tttatgaagactcaatagcaaatata	4156
Db	104463	ATATTTAATAAATAAATCAATTTTGTGTATTTATTTTAAATAAATAAATAAATAA	104404
QY	4157	cgaactttcagctcttagaaagcgtgctataatcattcagctgttagcttgagcga	4216
Db	104403	ATTAATAATAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	104344
QY	4217	ttctt 4221	
Db	104343	TTTTT 104339	
RESULT	10		
LOCUS	AE001398/c	14867 bp	DNA
DEFINITION	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.	INV	06-NOV-1998
ACCESSION	AE001398		
VERSION	AE001398.1	GI:3845197	
KEYWORDS			

SOURCE	malaria parasite P. falciparum.
ORGANISM	Plasmodium falciparum
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
AUTHORS	1 (bases 1 to 14867) Gardner,M.J., Tettelin,H., Carucci,D.J., Cummings,L.M., Aravind,L., Koonin,E.V., Shallow,S., Mason,T., Yu,K., Fujii,C., Pederson,J., Shen,K., Jing,J., Aston,C., Lai,Z., Schwartz,D.C., Petee,M., Salzberg,S., Zhou,L., Sutton,G.G., Clayton,R., White,O., Smith,H.O., Fraser,C.M., Hoffman,S.L. et.al.
TITLE	Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum
JOURNAL	Science 282 (5391), 1126-1132 (1998)
MEDLINE	99021743
REMARK	Erratum: [[published erratum appears in Science 1998 Dec 4;282(5395):1827]]
REFERENCE	2 (bases 1 to 14867) Gardner,M.J.
AUTHORS	Direct Submission
TITLE	Submitted (02-NOV-1998) The Institute for Genomic Research, 9712
JOURNAL	Medical Center Drive, Rockville, MD 20814, USA
FEATURES	Location/Qualifiers
source	1..14867 /organism="Plasmodium falciparum" /db_xref="taxon:5833" /chromosome="2" complement(1570..2424) /gene="PF0490c" complement(1570..2424) /gene="PF0490c" /note="predicted by GlimmerM" /codon_start=1 /product="hypothetical protein" /protein_id="AAC71887.1" /db_xref="GI:3845198" /translation="MKEKNEKIMDYLCPLDDVDREKSGKSNLLKSSSTKSDYKK SIFSKKRDSSHKSGFRGSGFNRKSGSPKKPYNNRLKNKNYNGRNFHNR DNFKRTSGRFDNRDGFSPKRRFISNRNKSYSKVSNGSNMGRSPKAPTSR TVVTLNNYKTVSAPVKFNLNLSLYRKNRTEALNTRKSPGVGTIKSSVPKRRIK GLKGSLSKTRKSTSGSKFPLNLYFLSKIRIVTSLNKLPSPLKQKNTEVNLPSL NNATTKN" 11241..14606 /gene="PF0495w" 11241..14606 /gene="PF0495w" /note="predicted by GlimmerM" /codon_start=1 /product="hypothetical protein" /protein_id="AAC71888.1" /db_xref="GI:3845199" /translation="MFAKKNTVREGFVNICFSYKKLYLKNFVTVNLNFEVNNKRR TNKIVKSKAQLFDKGLNIHDKLILFNLPKPKYKCAKCEISAKEVYKLLDEYKK FNVISLDIIQSVKIFDELDKTFTDYNFIEVKNIDKNVLNINIEYFNKNDITFHR ELIGKTCNKIMSYIHEMGNELIHFLIYFERNKNDKNLILFVYFNVFVDFHMYLFR HEIYKLLFFNFYLNNSNIPNKNLIQEMENLYFREIKNEKNYIKNKKEIYK CPAKFENVHDHNEKILNRLYVDNSILDDINNMCLNCLNNDINENIEIISKLL NFYCTILKKKGKNDNMTYKKEVIACTHILCDTKNTECFSDIDYSTLNSLNK FILNKIDKNFILFVECLLIKILNKFVNSQISLISLKNYIYILNNVYIVANN LFNDIMKFSYLCNIFLGKRIKTENENAVLIITHNDOTNYSNKENIKDIIQKRIEY IFYKNEYKDFHFKLSDLSLSIKLSNTFVKINEVNSYDFVLFNNISCLINFLV NNSVKYKDTYIYLNDLSFYKIKNDNRKKKKNFLLSSMKELCKNLLSVN RYIKHLHEEDNFQDKQYVCTFLNNFFDKLIHPHYIYNLMCHYKITYNFKCNKL INEDIISLLLTCSKQFYFIENNSDRYCKELIHLKYNIDDLKNYNTKYSID NISKIFISLSNKSQYTCVENALLLESQSEFKVTSTKGGIHMNDLNNNSID KYEHYIEYKKNLFINLKIIECLIKLNFILYKKKTYLYLKSLQPINENIL KKILYIANLYWEMGYCYCEMLERVLSSHKEQNLFSYANKVEMKMDKILCHISE DDYIEMSTMYVLFYDLKNINERQSNIRNNSNDRIDEIKKKYKLNNTLKH NNVKNYKSNNSNGNISNLKDDKNHNHNVEMDLIDNKNENKIKIOEGQNGENEN CKDVLVNDINIFGLMEKKKFLFFQLMYLNCNITKFKRRYVSSSLPFHMDVFKIK DMNLKYLLENYKIKNECAFLYTIIDIVLFKER"
gene	11241..14606 /gene="PF0495w"
CDS	11241..14606 /gene="PF0495w" /note="predicted by GlimmerM" /codon_start=1 /product="hypothetical protein" /protein_id="AAC71888.1"
gene	11241..14606 /gene="PF0495w"
CDS	11241..14606 /gene="PF0495w" /note="predicted by GlimmerM" /codon_start=1 /product="hypothetical protein" /protein_id="AAC71888.1"
BASE COUNT	6284 a 1019 c 1106 g 6458 t
ORIGIN	

revised: new gene prediction"

```
/codon_start=1
/product="hypothetical protein, PFC0582c"
/protein_id="CAB90286.1"
/db_xref="GI:7711067"
```

Query Match	2.4%;	Score 128.4;	DB 33;	Length 86827;
Best Local Similarity	44.6%;	Pred. No. 4e-07;		
Matches 987;	Conservative 0;	Mismatches 1196;	Indels 31;	Gaps 11;
QY 1831	tttacaaatgatttggtaataaacaatcccaatagttcacatcgataaacaacagattataaatt	1890		
Db 41525	TTTAAAAATATTATATATATATATATATATATATATATATATATATATATATATATATAT	41466		
QY 1891	acttaactcacagcgataattacccttccattgaagctacacaaacgggagatccta	1950		
Db 41465	TTCAAATTTAAATATTTATATATATATATATATATATATATATATATATATATATATAT	41406		
QY 1951	cagaagctgtagaacaagaattcataatgtataaataattatttagaaaaatggaattt	2010		
Db 41405	TATATTTTGTATATAAATAATATATATATATATATATATATATATATATATATATATAT	41346		
QY 2011	cagcagaatatttagaagtgcaaatataaagtaaaagcacattttaacttatgcatttg	2070		
Db 41345	TAAATTTAGCAATTTATTAATTTAAATTTATATATATATATATATATATATATATATAT	41286		
QY 2071	acggac-taaccttcatacatattttatggcatcctcaatactagaggacgcgcta	2129		
Db 41285	AAATACACATCAATAAATAATCATTTTATAAATAAATAAATAAATAAATAAATAAATAA	41226		
QY 2130	tcagaatcagtaatttacgataccatagacaaagtagtaatccaaatgtttaactcc	2189		
Db 41225	TATATATATATATATATATATATATATATATATATATATATATATATATATATATAT	41166		
QY 2190	gctatggaataatcttccaaacatatagaatttaacccgggcatctattaccctaatga	2249		
Db 41165	TACATATATAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA	41106		
QY 2250	gaatagttatgagaacatatgtgtcacacattatgttattgtttctttcattcaata	2309		
Db 41105	TAA-----ATATAAATATATAATATATATAAATATATAAATTAATTTCAATAAATA	41051		
QY 2310	catatgcaaatgatctcaatttaacataaagaagaagctcaacataaaataaaatacact	2369		
Db 41050	ATTAAATACATATATAAATAAATAAATTTTAAATAAATAAATAAATAAATAAATAAATA	40991		
QY 2370	atctatattgtgaacatcaataacctaccacaatttcccttaaaatttg--cattcaagaa	2427		
Db 40990	ATATATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	40931		
QY 2428	agcagatagccttatgatgcctttgataagcagagacttgcatactttacatcaaaaat	2487		
Db 40930	ATTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	40871		
QY 2488	attaaacgaaggatcaaaaaaacatctgctcagtttttgcacaacaattagaaggcaa	2547		
Db 40870	AATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	40811		
QY 2548	aggtatagacttaaaatttgatatagccctagacaatttttatatcatcataaaacccct	2607		
Db 40810	TATATTATTAAATTAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	40751		
QY 2608	atcagaaaactttgagaagcccttagtttactcagtgatgcatattcaaacccgtcac	2667		
Db 40750	ATATTATTAAATTAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	40691		
QY 2668	agatcaagaataattcaatagaataatagcagacagattgcacatgtaaaatcattata	2727		
Db 40690	TAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	40631		
QY 2728	ttctgctcctgaatttatagctacacaagaagaatgaatcacgcgtatatattcaaggccacc	2787		
Db 40630	TTAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	40571		

QY 2788	atattctaacaagtttcaaggacattaaatacaatacaataatcaaccaggaaacgct	2847		
Db 40570	AAATTT-AAATAAATATATTAATAATAAATACTTTAAATAATAAATAAATAAATAAATA	40512		
QY 2848	tcattatatataaaaaatagttttgacaaggaacaaaatcgtttatcagcgcagcaggaga	2907		
Db 40511	AATATTAAATTAATAAATAAATACTTAATAAGTATATAATAAATAA-----ATTAAATATA	40458		
QY 2908	tgtagatccaacacagctatcaaatcttactagataaataattcttccaaatcgccatc	2967		
Db 40457	TTTAATTAATAATTAATTAATTAATAAATAAATAAATAAATAAATAAATAAATAAATA	40398		
QY 2968	tgttaatacaaaaaatcaccatccagatcagctgtttaaataagagaacacattattata	3027		
Db 40397	AAAGTTAAAAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	40338		
QY 3028	tgtacagagagatgtaccacaagtgctaatgttggctacagacacacagtcaccatata	3087		
Db 40337	T-TATAATAATAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	40279		
QY 3088	cagcaagactatcatcgatcaaaacttgctcaactatgctagcgcgatttaagctcctaa	3147		
Db 40278	TTATAATAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	40219		
QY 3148	ttcaatatta--atgatagaatttaagagacaagttaggatttaacataccatagtagcagt	3205		
Db 40218	TTTAATAATACGTGTGTGAATATATATATATATATATATATATATATATATATATATCA	40159		
QY 3206	tcactatcacaatgaatcatcagtaagtgtctattgg-----tacaatattcactga	3258		
Db 40158	TAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	40099		
QY 3259	taataccacagtaacaaaatgtatatcccttaacagatatattatagagcacataaaaa	3318		
Db 40098	TATAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	40039		
QY 3319	gtatggagttgatgagacacttttgcaattgcaaaatcctagattaccacactctttat	3378		
Db 40038	TTATTATATTAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	39979		
QY 3379	tttactatggttaataacaataatgtttagtgagatattgtttaag-cttacaattcacag	3437		
Db 39978	TTTAATTTTATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATG	39919		
QY 3438	atctagatccgagttatatataataacatacaattcttactacaaagcaatacaaatagaag	3497		
Db 39918	AATTAATAATGTTATTATATAATTAATAAATAAATAAATAAATAAATAAATAAATAAATA	39859		
QY 3498	aagtataaataaattgccaagaaaaatttatctaagtaagtaataaattggaagtggaa	3557		
Db 39858	AAATATTATTATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT	39799		
QY 3558	aaacaataacaataaaggcaacaataatagatgctaaaaaacacacacaccttgggttaagta	3617		
Db 39798	TTATTATTTTATTATTAATATATATTTATTTATTAACGCTTATTTAATTCATTTAAT-39738			
QY 3618	tacaggttattgtatttactacaagtatctctattaggttatttaagtaagtaagtag	3677		
Db 39739	TAAATATATATATATTAATTTGAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATAA	39680		
QY 3678	cttcaatcaataaaaaaacatttaacccaagtgtagctcaccggagagccttattata	3737		
Db 39679	AACATTTATTATTATTTAAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTATT	39620		
QY 3738	agctttaacctggggaataatgaagcttttgcataatggttaagcaaaaaatttagtaacac	3797		
Db 39619	GAATATTATTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT	39560		
QY 3798	aatatcaaaattttctttacagagattatattgagccctacacataacaacattatttagaa	3857		
Db 39559	AAT----TATTATTATTATTATTATTATTAAATAAATAAATAAATAAATAAATAAATAAATA	39504		

Qy 1074 ccagcagtcagcacatggtattatacaaaagtcggtggaaactgatgatccagtaggatac 1133
Db 38158 ACGATTTAAAGTTTAAAGAAATTTACTATATTTATTAATAATAATATTTTAAATTAAC 38217
Qy 1134 tctggattagcacatcttttttgaacacttaagttttagtggaaacagaaaaatttcctcaat 1193
Db 38218 TTTTTCATAAAGAAATATATAGTGTGAATATGCAAAAAAACAACAAAAATGAAATTT 38277
Qy 1194 ctcacagcacacttagtaatataggcggaatttcaatgcaagcacactctcaatttgt 1253
Db 38278 CATATTTATAACATAATGATAAGTTTATAATAGGAACCGGATTTATAATAAAGTATT 38337
Qy 1254 actatactactcgaattaataaccaaaacaattatttctcttgcaatggatattga--at 1311
Db 38338 CATGTAATAATCTCCATAAATGAACAATGCTCTTGTGTTTTTGTGACATGTTTCATCAA 38397
Qy 1312 cagacegaatgcagaatttttaaggttaccgcgaagcatttaataagagcaacaaaggtag 1371
Db 38398 ATAAATAAAGAAATATTTTATAATAAATAAATAATGATATACACCATCATGATAAATAA 38457
Qy 1372 tcttagaagaagaataagatgagatgaaagcccaagcaaaaaacatactagaagaagaaa 1431
Db 38458 ATATAACTTAAATAATAATATTTTATACAAAGACAGCATATATAAAGGGAAATGA 38517
Qy 1432 tggaaaatgcattttattacaaatggatggcagaccagtagtaggagtggaacatgaaa 1491
Db 38518 ATATTAAAGAACCTTTTCATTAATCTTTAAGTATTATATAATTTATGTTTACCATACG 38577
Qy 1492 ttagaacactaca-acaaagaagttgctgaagcccttcaatgaagctacattatagtcctaat 1550
Db 38578 ACAAAAATCATACACATCTTTATGTATTATGAAATTAAGAAAATCAAAAAGTACTTTTACA 38637
Qy 1551 aatgctataattaagttaactgagatgcagatccacaagaagtaatacacacttgcaaaa 1610
Db 38638 AAGATAAAGGAAATAAATAAATTTTATTTATCCATTAATAGTTTTCACATTCAAAAGA 38697
Qy 1611 caatcactatggaaaataccatcctaataataagaacccctcaagctgaagttgagtagaa 1670
Db 38698 AAAATTACTTAAATTTATGTACCCCTAATGTTAAATTTCTAATTAAGTTTACAAAATAAATATA 38757
Qy 1671 ccacgcataaacaataatgatctttaacataataaagacagttcagtagaatacccgaaa 1730
Db 38758 TATATAGTATAAAGAAATTAAGAACATATATTTATTTATATATACATTTTTTTTATTAAT 38817
Qy 1731 ctgttttaagtatccaataccaaatggattaccacaataaaaaactacatacttaaacatg 1790
Db 38818 TATTAAATATAAATAATTTTATATACAAATATAAATCAATGCTTTTAAATAAATATA 38877
Qy 1791 atgttagcagaataactcgttagtggtgtaattccagccctgctttcaaatgattggtaatt 1850
Db 38878 TAAATTTTATTAATATAAATAATAAATTAAGTATTATTTATATGTTATATAATACATTTTATTTTA 38937
Qy 1851 acaatcccaatagttacatcgcataaaaaacagattataattacttaactgacagcgataat 1910
Db 38938 ATTCTTTCTAATTTAATATGATAACATATTTTATAATTAATTTTACACATTTATATAAA 38997
Qy 1911 tacctttccattgagctcat--accataaaacgggatctctacagaagctgtagaacag 1968
Db 38998 AACAATTAATTAATAATTAATTTTATTTTAAATAAATAAATAAATAAATAAATAAATAA 39057
Qy 1969 aaattcataaattgtataaataattatttagaataatggaaatttcagcagaataatttagaaa 2028
Db 39058 TAAATAAAAAAATAATATGTAATAGTTATATATAATAATTAATAATTAATAAATAAATAA 39117
Qy 2029 gtgcaagtataaagaataaagcacatttaactatgctatttgacggcaggaacttccat 2088
Db 39118 TAAATAATAAATAAATAAATAATATATATTTAAATAAATAAATAAATAAATAAATAAATA 39177
Qy 2089 catatttttagcgtcatctcaactacagagtagtaccgctcatcagaataatcagtaatttt 2148
Db 39178 AATTATTTTAAATTAATTAATAAATAAATAAATAATATTTATTTAAATAAATAAATAAAT 39237
Qy 2149 acgataccatagacaaaagtaagatcccaagatggttaactccgctatggaaaatactcttc 2208

Db 39238 ATATATTTATTTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 39297
Qy 2209 aaacaataataagataaacccggcatttattacctaagtggagaaatagttatgagaacat 2268
Db 39298 TTATATATATATTTATTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 39357
Qy 2269 attggttacacatttaattgattttcttttccatcaatacatatgcaaatgatctcaa 2328
Db 39358 AATAAATTAATAATATATTTATTTTAAATAAATAAATAAATAAATAAATAAATAAATAA 39417
Qy 2329 tattaacataaagaagctcacactaaataaaaaatacacatactctatctatgttgaacatca 2388
Db 39418 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 39476
Qy 2389 taacctaccacaatttccttaaaatttgcattcaagaagcaggatcacactcatgatgc 2448
Db 39477 TTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 39536
Qy 2449 ctttgataagcaaggacttgcatactttacatcaaaaaatttaaacgaaggaacaaa--a 2506
Db 39537 ATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 39596
Qy 2507 acaactatgctctcagtttgcacaacaattagaagcgcaaggtatagacttaaaattt 2566
Db 39597 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 39656
Qy 2567 gatatagacctagacaatttttatatatcatcttaaaaaaccccttatcagaaaaactttgaaga 2626
Db 39657 ATAATTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 39716
Qy 2627 gccctagtttactcagtgatgcataattcaacacocgcagatcagaagaataattcaat 2686
Db 39717 TCAAAATTAATAATATATATTAATTAATGAATTAATAAAGCAGTTATATAAATAAATA 39776
Qy 2687 agaataatagcagaacagattgcacatgttaaacattatattctgctcctgaatttata 2746
Db 39777 ATATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 39836
Qy 2747 gctacaacagaatgaatcacgcgtatattcaagggcaccatattcctaacaagaatttac 2806
Db 39837 ATAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 39895
Qy 2807 gggacattaaatacaatacaataatcaacacaggaagacgttgctgctatataataaaaaat 2866
Db 39896 AATATTATAATAACATTTTAATTCATATAAATAAATAAATAAATAAATAAATAAATAAAT 39955
Qy 2867 agtttgacaaggaacaaatcggttatcagcgacgagagatgtagatccaacacagcta 2926
Db 39956 AATTTAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 40012
Qy 2927 tcaaatctactagataaataatattcttccaaattgcatctggtgaatacaacaaataacc 2986
Db 40013 AATTTATTAATTTAATAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 40072
Qy 2987 ataccagatacagctgttaataagagagacacattattatataatgcagagagagatgtaacca 3046
Db 40073 ATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 40132
Qy 3047 caaagtgtcataatgttgcacagacacagatccatatacacagcaaga----- 3096
Db 40133 TGAACATATTTTATTTTAAATTTTGAATACAAATAAATAAATAAATAAATAAATAAATAA 40192
Qy 3097 --ctatcatgcatacaaatctgttccaatactatgctagcggaattgaagctccaatccaata 3154
Db 40193 ATATATTACACACACGATTTATTAATACTGTTTAAATTTAAATTTAAATTTAAATTTAA 40252
Qy 3155 ttaatgatagaattaa---gagacaagttaggattaaacataccatagtagcagttcacta 3211
Db 40253 ATTTATTTATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 40312
Qy 3212 tctaacatgaatcatagtaagtgtgctatttggtaacaatttcactgataataaccacagta 3271

[illegible]

Qy 2049 gacatttaacttgacgttgaacgactaaacttccatactatattttat-----gg 2101
 Db 2215 TTTTTTAAAAAATAATTTTTTAAAGTTTTTAATATATAATAAATTTATGAATAGGG 2156
 Qy 2102 catgatcctaactactaggagtagccgctacagaaatcagtaatttaccagatccatag- 2160
 Db 2155 GAATAAATTTATTTCAATTTTACATATATATATATATATATATATACAAATTAAT 2096
 Qy 2161 aceaagtaagtcacaaagtgttaactccgctatggaaaatctcttccaaacaataaa 2220
 Db 2095 TCAGATTTAGTCATTAATAATAAATTTATTTATTAATTTATTAATTTAAATGAAATTA 2036
 Qy 2221 gattacccgggcatatttaccctaagtgagaaatagttatgagaacacatatgtgttacac 2280
 Db 2035 AATTATATGATATATATAATAATATATGAATTTTATTAATAAATCAATTTTAAAT 1976
 Qy 2281 attaatattgatttcttcttccatcaatcatatgcaaatgcatcacaattataacataaa 2340
 Db 1975 TTTTATATATTAATAAATAATTTTATTAATTTTAAATAAATTTTATTTATTAATAATAT 1916
 Qy 2341 agaagctcaacta-----aaaataaaatcacactatctatgttgaaacatcata 2390
 Db 1915 TTATTATAAAAATAGTTTATTAAGTATATTTAATAAATCAATTTTAAAAAATAA 1856
 Qy 2391 acctaccacaatttctctaaatttgcattcaagaagcaggatagcgttatgatgct 2450
 Db 1855 TATTTTTTAAAGTTTTTAAATATATACAAATAATTTATGAATAGGGGAATAAATTTTCA 1796
 Qy 2451 ttgataagcaaggaacttgcatacttaccatacaaaatattaaacgaagatcaaaaaa 2510
 Db 1795 TTTTATATATATATATATATATATATATATATATTTTCAGATTTAGTGATTAATAATA 1736
 Qy 2511 actatgctctcagtttgcacaa--caattagaaggcaaggtatagacttaaaatttga 2568
 Db 1735 ATATTTTATATATATATATATATTTAATTTAAGTAAATTTAATAATATATATATA 1676
 Qy 2569 tatagacta-----gacatttttatatatcatcattaaacottatcagaagaacttgaag 2624
 Db 1675 TATAAATAAATTTGAATTTTTTAAAAATATATTTTAAATTTTTTATATATAAATAAT 1616
 Qy 2625 aagccctagtttactcagtgatgcataattcaacacgcgcagacatcaagaataattca 2684
 Db 1615 TCTTATTAATTTTAAATAATTTTATTTAATAATAATTTATTAATAAATAAGTTTAT 1556
 Qy 2685 atagataatagcagaacagattgcacatgttaacattatcttcgctcgtgaattca 2744
 Db 1555 TAAGTATATTAATAAATAATTTTTTTTTAAAAAATAATTTTTTAAAGTTTAAATTA 1496
 Qy 2745 t-----agctacacagaaatgaatcgcgttatattcaaggcgaccattcttaac 2797
 Db 1495 TATAATAAATTTATGAATAGGGGAATAAATTTTATTTTCAATTTTACATATATATATAT 1436
 Qy 2798 aaagtctcgggacattaaatacaatcaataatacaacacaggaagacgttcattatat 2857
 Db 1435 ATATATATATACAAATAATTTAATTCAGATTTAGTGATTAATAATAATTTATTTATATAC 1376
 Qy 2858 ataaaaaatagtttgacaaagcaacaaatcggtatcagcgacgagagatgatagacca 2917
 Db 1375 TTATATAATTTTAAATTTGAAAAATTAATTTATATATATATATATAATAATGAAT 1316
 Qy 2918 acacagctatcaaaatttactagataaaatatattcttccaaattgcccactcgtggaataac 2977
 Db 1315 TTTTATAA--AAATCAATTTTAAATTTTATATATATTAATAAATAATTTTATTAATTAAT 1259
 Qy 2978 aaaaatacattaccagatcagcgttgaatagagaagacacacattattatatgtacagaga 3037
 Db 1258 TAAAAATAATTTTATTAATAAATAATTTTATTAATAAATAAGTTTATTAAGTATAATTTAA 1199
 Qy 3038 gatgc-----accacaagtgcatatgttttgcagacacagcagaccata 3084
 Db 1198 TAAATCAATTTTTTTTTAAAAAATAATTTTTTAAAGTTTATTAATTAATAAATAATTTAT 1139
 Qy 3085 tcacagcaagactatcatgcatcaaacctgttctcaactatgctaggcggaattagctct 3144

Db 1138 GAATAGGGGAATAAATTTATTTTCAATTTTTTATATATATATATATATATATATAT 1079
 Qy 3145 caattcaatatttaattagatagaagaacagtaggattaaacataccatcagtagcag 3204
 Db 1078 TATTTTCAGATTTAGTGATTAATAAATAATTTATTTATATATATATATATTAATTA 1019
 Qy 3205 ttcaatatcaatcaatcaatcatagtaagtgtctatttgggtacaaatattcactgataatc 3264
 Db 1018 ATTAATAATATATATATATATATATATAATAATAAATTTGAATTTTAAAAAATTAAT 959
 Qy 3265 caca---gtacacaaatgtatatccgctcttaacagatatattatagagcacattaaaaagta 3321
 Db 958 TTAATTTTATTAATAAATAAATAATTTCTTATTAATTTTAAATAAATTTTATTTATAA 899
 Qy 3322 tggagttgatgaagcacacttttgcatt-tgcacaaatcctagttattcccaactctttttt 3380
 Db 898 AATAATTTATTAATAAATAAGTTTATTAAGTATATTAATTAATAAATAAATTTTAAAAA 839
 Qy 3381 tatctatgttaaatcaacaatattgtttagtgagatttggtaaagcttacaattcacogate 3440
 Db 838 AAAAAATACTTTTTAAGTTTTTAATTTATATATAAATAAATTTATAGGGGAATAAATTTAT 779
 Qy 3441 tagatccggagttatattataaatacaaatcttactacaagaacatacaatagagaag 3500
 Db 778 TTTTATTTATTTATGATATATATATATATATATATATATATATATATATA-TATATA 720
 Qy 3501 taataataaattgccagaataattttctcaatgaattagtaaatctgaagtaggaataa 3560
 Db 719 TATATAAATTTTTCAGATTTAGTGATTAATAAATAATTTATTTATTTATTTATTCGTA 660
 Qy 3561 acaataacataaattggcaacaaatagatgctcaaaaaacacacactcgttgtaagtatac 3620
 Db 659 TAATTTAATTAATAATCAAAATTTATTTATATATATATATATTTGATTTTAAATAAATTTAT 600
 Qy 3621 aggttattgtatttact-acaagttattctttaggttatttaagtaagataagtagct 3679
 Db 599 TACTTTTTTTTATTTATTCATAAAAAATTTTAAATAATTTTTTTTAAATAGATTAATTTTCA 540
 Qy 3680 tcaatcaataaaaaaacetttaaccaagtggttagctctcacggagagctctattataag 3739
 Db 539 TTTTGTGTAATAAATAATATTTTTTAATAATAATTTTCAATTTTTTTTAAAAAATAATTTT 480
 Qy 3740 ctttaacctgggataataatgaagttttagcttaagtgttaagcaaaaaatttagtaatac-- 3797
 Db 479 TTTAAAAATTTATATTTATATATATTTTTTAAAAAATTTGTAATAAATAAATTTTAAAAAT 420
 Qy 3798 -aatatcaaaatttcttctacaggaattatttgcacctaccatacaacattattattaga 3856
 Db 419 AAAAAAATAAATTTTTTTTAGTCATTTAAAGAAATAATTAATCTATAATTTTTTAAAAAT 360
 Qy 3857 aaatgacacagatcacacacatacaataaattatcactacaattcaattataaacaatg 3916
 Db 359 TTAATAAATAAATAATTTTTTTAAAAAATAATTTTTTTTAAAAAATAATTTTAAAAA 300
 Qy 3917 agtatttttacttaattattatttttttttttttttttttttttttttttttttttttttt 3976
 Db 299 AAGTGTAAAAATTTTAAATTTTAAATTTAAAAATTTAAATTTTATTATTATTAATATTGAT 240
 Qy 3977 caataa 3982
 Db 239 AAATTA 234

RESULT 15
 DMU37541/c
 LOCUS
 DEFINITION Drosophila melanogaster complete mitochondrial genome.
 ACCESSION U37541
 VERSION U37541.1
 KEYWORDS GI:1166529
 SOURCE Drosophila melanogaster.
 ORGANISM Mitochondrion Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 12511 to 12682)
Clary,D.O., Goddard,J.M., Martin,S.C., Fauron,C.M. and Wolstenholme,D.R.
Drosophila mitochondrial DNA: a novel gene order
Nucleic Acids Res. 10 (21), 6619-6637 (1982)

2 (bases 5269 to 5695)
Clary,D.O., Wahlethner,J.A. and Wolstenholme,D.R.
Transfer RNA genes in Drosophila mitochondrial DNA: related 5' flanking sequences and comparisons to mammalian mitochondrial RNA genes
Nucleic Acids Res. 11 (8), 2411-2425 (1983)

3 (bases 404 to 5272)
de Bruijn,M.H.
Drosophila melanogaster mitochondrial DNA, a novel organization and genetic code
Nature 304 (5923), 234-241 (1983)

4 (bases 804 to 1778)
Satta,Y., Ishiwa,H. and Chigusa,S.I.
Analysis of nucleotide substitutions of mitochondrial DNAs in Drosophila melanogaster and its sibling species
Mol. Biol. Evol. 4 (6), 638-650 (1987)

5 (bases 5268 to 13619)
Garesse,R.
Drosophila melanogaster mitochondrial DNA: gene organization and evolutionary considerations
Genetics 118 (4), 649-663 (1988)

6 (bases 441 to 2967)
Satta,Y. and Takahata,N.
Evolution of Drosophila mitochondrial DNA and the history of the melanogaster subgroup
Proc. Natl. Acad. Sci. U.S.A. 87 (24), 9558-9562 (1990)

7 (bases 14215 to 14512)
Ballard,J.W., Olsen,G.J., Faith,D.P., Odgers,W.A., Rowell,D.M. and Atkinson,P.W.
Evidence from 12S ribosomal RNA sequences that onychophorans are modified arthropods
Science 258 (5086), 1345-1348 (1992)

8 (bases 14917 to 19517)
Lewis,D.L., Farr,C.L., Farquhar,A.L. and Kaguni,L.S.
Sequence, organization, and evolution of the A+T region of Drosophila melanogaster mitochondrial DNA
Mol. Biol. Evol. 11 (3), 523-538 (1994)

9 (bases 1 to 408; 13319 to 19517)
Lewis,D.L., Farr,C.L. and Kaguni,L.S.
Drosophila melanogaster mitochondrial DNA: completion of the nucleotide sequence and evolutionary comparisons
Insect Mol. Biol. 4 (4), 263-278 (1995)

10 (bases 1 to 19517)
Lewis,D.L., Farr,C.L. and Kaguni,L.S.
Direct Submission
Submitted (03-OCT-1995) Laurie S. Kaguni, Biochemistry Department, Michigan State University, East Lansing, MI 48824-1319, USA
Location/Qualifiers
1. .19517
/organism="Drosophila melanogaster"
/organelle="mitochondrion"
/db_xref="taxon:7227"
/note="derived from new and previously submitted sequences; sequence is a composite containing sequences obtained from different Drosophila melanogaster strains"

1. .65

trna

/product="trna-Ile"
complement(97. .165)
/product="trna-Gln"
171. .239
/product="trna-Phe"
240. .1265
/codon_start=1
/transl_table=5
/product="NADH dehydrogenase subunit 2"
/protein_id="AAC47811.1"
/db_xref="GI:1166530"
/translation="MFNNSKILFITIMIGLITITVTSNWLGAWGLINLLSFPL
LSDNNLMEASLKYFLQVLASTVLFSSILLMLKNNMNEINFSMIIMSALL
LKSRAFFHFWFNMMEGLTWMLMTWQKIAPMLISYLNKIKLISVILSVII
GAIGLQNTSLRKLMAFSSINHLGWLSSIMISEIWLILFFYSFLSVLTFMFNIF
KLFLNQLFSWFVNSKILATFLFMNFLSIGGLPPFLGFLPKWLVIQQLFLCNOYFWLT
IMMSTLITLFFYLRCISAFMNYFENNWMNNNSINNYNIMTIFESIFGLFLI
SLFYFMF"
1264. .1329
/product="trna-Trp"
complement(1322. .1383)
/product="trna-Cys"
complement(1403. .1468)
/product="trna-Tyr"
join(1470. .1472,1474. .3009)
/codon_start=1
/exception="mechanism underlying reading frame shift after first codon uncertain"
/transl_table=5
/product="cytochrome c oxidase subunit I"
/protein_id="AAC47812.2"
/db_xref="GI:7412849"
/translation="MSRWLFSTNKHDKIGTYLFGAWAGMVGTSILIRAEGLHGP
ALIGDDIYNVIVTAHAFIFMFMVMPIMIGGFNWLVLMLGAPDMPMNMMSFW
LLPALSLLVSMVENGAGTGWYPPPLSAGIAHGASVDLALFSLHLAGISSILGA
FPPATVNNRSTGISLDRMPLFVWSVITALLLLSLPLAGAITMLTDRNLTSF
FPPAGGDPILYOHLFHFFGHPEVYILIPFGMISHIIISQESKKETFGSLGMIYAM
LAIGLGFVWAHHMFTVGMDVDTRAYFTSATMIIAVPTGKIFSLATLHGTQLYS
PAILWALGFVLTFTVGGTGVLANSSVDIILHDYTVVVAHFVYLSMGAVFIMAGF
IHWPFLTGLTLNNKWLKSHFIMFIGNLTFPPQHFGLAGMPRYSPYDAYTTWN
IVSTIGSTISLLGILFFFIWESLSVQRQVYPIQLNSSIENYQNTPTAEHSYSELP
LUTN"
3012. .3077
/product="trna-Leu"
3083. .3767
/note="TAA stop codon is completed by the addition of 3' A residues to the mRNA"
/codon_start=1
/transl_except=(pos:3767,aa:TERM)
/transl_table=5
/product="cytochrome c oxidase subunit II"
/protein_id="AAC47813.1"
/db_xref="GI:1166532"
/translation="MSTWANLQDSASPLMEQLIEFHDHALLILYMITVLVGLMFM
LFNNYNNRFLHGOIEMITLIPAILLLFALPSLRLLYLLDEINFSVTLKSLGH
QWTSYEYSDFNNEIDSYNIPTELMDTGRLLDNDVNLVLPMSOIRILYTAADV
HSWTVPALGVKVDGTPGRNLQTNFFINRPGLYGQCSEICGANHSFMPVIESVPVNY
FIKWISSNNS"
3768. .3838
/product="trna-Lys"
3840. .3906
/product="trna-Asp"
3907. .4068
/codon_start=1
/transl_table=5
/product="Atpase 8"
/protein_id="AAC47814.1"
/db_xref="GI:1166533"
/translation="MPQMAPISWLLLIIFSIITFILFCSINYSYMSPNPKSNELKNI
NLNSMNWKW"
4062. .4736
/codon_start=1
/transl_table=5

		/product="ATPase 6" /protein_id="AAC47815.1" /db_xref="GI:1166534" /translation="MMTNLFVSVDPLAIFNFSLNWLSTFLGLMIPSIYWLMPSRYNIMNSILLTHKEKTKLLGSPGHNGSTFIFLSFLINFNMGLPFYIFTSTSHLTLT LSIALPLWLCFMYLGWINHTQHFAHLVPOGTPAILMPMVCITSNIIIRPGTLAAR LTANMAGHLLLLLTGNTGSSMSYMLTFLMLAQIALLVLESAVAMIQSYVFAVLSTL YSSEVN" /codon_start=1 /transl_table=5 /product="cytochrome c oxidase subunit III" /protein_id="AAC47816.1" /db_xref="GI:1166535" /translation="MSTHSNHPHLVDYSPWLTGAIGAMTTVSGMKVWFHQYDISLF VLNIIITIVYQWRDVSREGYIQGLHTYAVTIGLRWGMILFILSEVLFFVFFWAF FHSLSPAIELGASWPWMIISFNPFQIPLLTAIALLAGVTVAHSHLMENHQSQT TOGLFTVLLGIYFTILQAVEYTEAPETIADSYGSTFFMATGFHGIHLVIGTFTLLV CLARLHNHFSKXHHGFGEAAANYHFVDVWVLFYITIIYWGG" /product="tRNA-Gly" /codon_start=1 /transl_table=5 /product="NADH dehydrogenase subunit 3" /protein_id="AAC47817.1" /db_xref="GI:1166536" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Ala" /protein_id="AAC47818.1" /db_xref="GI:1166537" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Arg" /protein_id="AAC47819.1" /db_xref="GI:1166538" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Asn" /protein_id="AAC47820.1" /db_xref="GI:1166539" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Ser" /protein_id="AAC47821.1" /db_xref="GI:1166540" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Glu" /protein_id="AAC47822.1" /db_xref="GI:1166541" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Phe" /protein_id="AAC47823.1" /db_xref="GI:1166542" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Leu" /protein_id="AAC47824.1" /db_xref="GI:1166543" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Ile" /protein_id="AAC47825.1" /db_xref="GI:1166544" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Met" /protein_id="AAC47826.1" /db_xref="GI:1166545" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Thr" /protein_id="AAC47827.1" /db_xref="GI:1166546" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Pro" /protein_id="AAC47828.1" /db_xref="GI:1166547" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Tyr" /protein_id="AAC47829.1" /db_xref="GI:1166548" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-His" /protein_id="AAC47830.1" /db_xref="GI:1166549" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Val" /protein_id="AAC47831.1" /db_xref="GI:1166550" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Pyl" /protein_id="AAC47832.1" /db_xref="GI:1166551" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Trp" /protein_id="AAC47833.1" /db_xref="GI:1166552" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Lys" /protein_id="AAC47834.1" /db_xref="GI:1166553" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Gln" /protein_id="AAC47835.1" /db_xref="GI:1166554" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-Asp" /protein_id="AAC47836.1" /db_xref="GI:1166555" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-IsoC" /protein_id="AAC47837.1" /db_xref="GI:1166556" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-IsoD" /protein_id="AAC47838.1" /db_xref="GI:1166557" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-IsoE" /protein_id="AAC47839.1" /db_xref="GI:1166558" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-IsoF" /protein_id="AAC47840.1" /db_xref="GI:1166559" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-IsoG" /protein_id="AAC47841.1" /db_xref="GI:1166560" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-IsoH" /protein_id="AAC47842.1" /db_xref="GI:1166561" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-IsoI" /protein_id="AAC47843.1" /db_xref="GI:1166562" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-IsoJ" /protein_id="AAC47844.1" /db_xref="GI:1166563" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-IsoK" /protein_id="AAC47845.1" /db_xref="GI:1166564" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-IsoL" /protein_id="AAC47846.1" /db_xref="GI:1166565" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-IsoM" /protein_id="AAC47847.1" /db_xref="GI:1166566" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-IsoN" /protein_id="AAC47848.1" /db_xref="GI:1166567" /translation="MFSIIFIALLIILLITIVFLASILSKKALIDREKSSPFECGFD PKSSRLPFSLRFLLTIIFLFDVEIALILPMIIMKYSNIMWITTSIIIFILLILI GLYHWNQGMNWSN" /product="tRNA-IsoO" /protein_id="AAC47849.1" /db_xref="GI:116
--	--	-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

Search completed: December 3, 2000, 00:11:50
Job time: 33425 sec

THIS PAGE BLANK (uspto)